

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 14:32:43 ; Search time 12601.5 Seconds
(without alignments)
17976.355 Million cell updates/sec

Title: US-09-497-957-1

Perfect score: 10825

Sequence: 1 TCTAAGGTGAGATAAAATT.....TCCCAAAATTTTCATAAAC 10825

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_to.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

1	10823	100.0	10825	6	AR117789
2	10823	100.0	10825	6	AR117790
3	10823	100.0	10825	6	AR117791
4	10823	100.0	10825	6	AR117792
5	10823	100.0	10825	6	AR149459
6	10823	100.0	10825	6	AR149460
7	10823	100.0	10825	6	AR149461
8	10823	100.0	10825	6	AR149462
9	10823	100.0	246240	6	AR036572
10	10823	100.0	246240	6	AR036573
11	10823	100.0	246240	6	AR036574
12	10759.8	99.4	12146	9	HSHE
13	10658.6	98.5	193752	2	AL359892
14	7542	69.7	246282	9	HSU01328
15	4251	39.3	101099	9	AL353759
16	2556.4	23.6	8622	6	AX347044
17	2248.8	20.8	8622	6	AX347045
18	1508.6	13.9	2115	9	HSAA04378
19	1421	13.1	1479	9	HSHLAA6
20	1407	13.0	4349	4	AF301592
21	1051.6	9.7	2727	9	HSU60319
22	1030.2	9.5	1885	9	AF144242
23	831.2	7.7	874	9	HSHLAH2
24	769.4	7.1	772	9	AF184234
25	740.2	6.8	3334	4	AF301591
26	701	6.5	701	9	HSAA298839
27	677.8	6.3	794	9	AF144238
28	657	6.1	761	9	HSHLAH1
29	638.4	5.9	653	9	HSHLAH4
30	560	5.2	560	9	HSAA298840
31	547	5.1	547	9	AF147392
32	546.8	5.1	551	9	AF331065
33	516	4.8	517	6	AR117804
34	516	4.8	517	6	AR117805
35	516	4.8	517	6	AR149474
36	516	4.8	517	6	AR149475
37	516	4.8	517	6	AR149475
38	516	4.8	517	6	AR149475
39	516	4.8	517	6	AR149475
40	511.6	4.7	526	9	HSHLAH7
41	430.2	4.0	987	9	AF150664
42	398.2	3.7	128726	9	AF136458
43	398.2	3.7	130195	2	AC090170
44	393.8	3.6	103259	2	AC012430
45	389	3.6	190112	2	AP002354

ALIGNMENTS

RESULT 1

LOCUS	AR117789	10825 bp	DNA	linear	PAT 16-MAY-2001
DEFINITION	Sequence 1 from patent US 6140305.				
ACCESSION	AR117789				
VERSION	AR117789.1	GI:14098695			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 10825)				
AUTHORS	Thomas, W.J., Drayna, D.T., Feder, J.N., Gnirke, A., Ruddy, D., Tsuchihashi, Z. and Wolff, R.K.				
TITLE	Hereditary hemochromatosis gene products				
JOURNAL	Patent: US 6140305-A 1 31-OCT-2000;				
FEATURES	Location/Qualifiers				
source	..10825				
BASE COUNT	2998 a 2253 c 2648 g 2926 t				
ORIGIN					

Query Match 100.0%; Score 10823; DB 6; Length 10825;

Best Local Similarity 100.0%; Pred. No. 0;				
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
QY	1	TC	TAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATAAATATTTA	60
DB	1	TC	TAAGGTTGAGATAAAATTTTAAATGATGATGAAATTTGAAATCATAAATATTTA	60
QY	61	AA	TATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACCCCT	120
DB	61	AA	TATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACCCCT	120
QY	121	TC	AGGATTTAAACCAAGGGGACACTGGATCACCCTAGTTTCAACAGCAGTACCTT	180
DB	121	TC	AGGATTTAAACCAAGGGGACACTGGATCACCCTAGTTTCAACAGCAGTACCTT	180
QY	181	CT	GCTCTAGGAGAGAGAACTAAAGTTCCTGAAAGACCTGTTGCTTTTCAACAGAGTT	240
DB	181	CT	GCTCTAGGAGAGAGAACTAAAGTTCCTGAAAGACCTGTTGCTTTTCAACAGAGTT	240
QY	241	TT	ACTGGGCACTCTCCTAGGCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCC	300
DB	241	TT	ACTGGGCACTCTCCTAGGCTAGGCAATAGCTGTAGGTGACTTCTGGAGCCATCCC	300
QY	301	TT	TCCCGCCCCAAAAGACGGAGATTTAAAGGGGAGCTCGCGCAGAGCTGGGAA	360
DB	301	TT	TCCCGCCCCAAAAGACGGAGATTTAAAGGGGAGCTCGCGCAGAGCTGGGAA	360
QY	361	AT	GGCGGGAGCGAGCGCGGGCTTCTCCTGATGCTTTTGCAGACCGGCTCTG	420
DB	361	AT	GGCGGGAGCGAGCGCGGGCTTCTCCTGATGCTTTTGCAGACCGGCTCTG	420
QY	421	C	AGGGGCGCTTGCTGCTGAGTCCGAGGGCTGGGGGCGAACTAGGGCGGGGGGTG	480
DB	421	C	AGGGGCGCTTGCTGCTGAGTCCGAGGGCTGGGGGCGAACTAGGGCGGGGGGTG	480
QY	481	GA	AAAAATCGAAACTAGCTTTTCTTTGGCTTGGGAGTTTGCCTAACTTTGGAGACCTGC	540
DB	481	GA	AAAAATCGAAACTAGCTTTTCTTTGGCTTGGGAGTTTGCCTAACTTTGGAGACCTGC	540
QY	541	TC	ACCTATCCGCAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGAGGAGTGC	600
DB	541	TC	ACCTATCCGCAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGAGGAGTGC	600
QY	601	CT	ACCTGAACCTCAGATAGGGTCCCTCGCCCCAGAGCTGCCCTTCCCCGGGTGT	660
DB	601	CT	ACCTGAACCTCAGATAGGGTCCCTCGCCCCAGAGCTGCCCTTCCCCGGGTGT	660
QY	661	CC	GGCTCTCGGGAGTGACTTTTGGACCGCCACTCCCTTCCCCCAACTAGATGCTTT	720
DB	661	CC	GGCTCTCGGGAGTGACTTTTGGACCGCCACTCCCTTCCCCCAACTAGATGCTTT	720
QY	721	TA	ATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCTGGGGCTCTTTGAACCTGG	780
DB	721	TA	ATAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCTGGGGCTCTTTGAACCTGG	780
QY	781	AA	CTGGGTTTATTTCCAACTGAGCTGAGTGTGAGTTCCTTCCCAAGTATCTCCAAACAG	840
DB	781	AA	CTGGGTTTATTTCCAACTGAGCTGAGTGTGAGTTCCTTCCCAAGTATCTCCAAACAG	840
QY	841	AA	GTTTCTCCCTGAGTGTGCTCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900
DB	841	AA	GTTTCTCCCTGAGTGTGCTCGGAGAGGCTGAGCAAAACCCACAGCAGGATCCGACGG	900
QY	901	GT	TTCACCTCAGAACGAATTCGCTTGGGGTGGGGGGCGGAAGAGTGGCTTGGGA	960
DB	901	GT	TTCACCTCAGAACGAATTCGCTTGGGGTGGGGGGCGGAAGAGTGGCTTGGGA	960
QY	961	T	CTGAATTTCCACATTTCCACCCACTTTTGGTGAGACTGGGGTGGAGGTCTCTAGGT	1020
DB	961	T	CTGAATTTCTTCCACATTTCCACCCACTTTTGGTGAGACTGGGGTGGAGGTCTCTAGGT	1020
QY*	1021	GG	AGGCTCTCAGAGAGGCTTACCTCGGGCTTTTCCCACTCTTTGGCAATTTCTTTT	1080

QY 2161 AAACCTTTGCCACATGTCACCTAGTAGACAAACCTCTCGTAAAGAGCTCGGGTTGAAAA 2220
DB 2161 AAACCTTTGCCACATGTCACCTAGTAGACAAACCTCTCGTAAAGAGCTCGGGTTGAAAA 2220
QY 2221 AATAAACAAGTACTGCTGGGAGTAGAGCCAAAGAAGTAGTAAATGGGCTCAGACAGGA 2280
DB 2221 AATAAACAAGTACTGCTGGGAGTAGAGCCAAAGAAGTAGTAAATGGGCTCAGACAGGA 2280
QY 2281 GCCAACAAGGTTGTGAGCGGCTGTAGGCTGTGGTGTGAATCTAGCCAAGAGTA 2340
DB 2281 GCCAACAAGGTTGTGAGCGGCTGTAGGCTGTGGTGTGAATCTAGCCAAGAGTA 2340
QY 2341 ACAGTATCTGTACACAGGCTTTTAAAGATTGCTCTGCCTGCTATGTGGAAGCAGAAATG 2400
DB 2341 ACAGTATCTGTACACAGGCTTTTAAAGATTGCTCTGCCTGCTATGTGGAAGCAGAAATG 2400
QY 2401 AAGGGACACAGTAAACAGCGGAGCCAGCCAGGAGAGCTGTACACAGTCCAGGCAAG 2460
DB 2401 AAGGGACACAGTAAACAGCGGAGCCAGCCAGGAGAGCTGTACACAGTCCAGGCAAG 2460
QY 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCTGAA 2520
DB 2461 AGGTAGTGGAGTGGGCTGGGACAGAAAGGGAGTGACAAACCATTTGCTCTCTGAA 2520
QY 2521 TATATTCTGAAGAAAGTCTCTGAAGATTCTATGTTGTGAGAGAAAGAGAAATGG 2580
DB 2521 TATATTCTGAAGAAAGTCTCTGAAGATTCTATGTTGTGAGAGAAAGAGAAATGG 2580
QY 2581 CTGGGTAGTAGCTCATGCCAAGAGAGAGGCCAAGAGAGCAGATTCTGAGCTCAGGA 2640
DB 2581 CTGGGTAGTAGCTCATGCCAAGAGAGAGGCCAAGAGAGCAGATTCTGAGCTCAGGA 2640
QY 2641 GTTCAAGCAGAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
DB 2641 GTTCAAGCAGAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGGTGGCATGCACCTGTATCTAGCTACTCGGAGGCTGAGGTGAGGGTA 2760
DB 2701 GCTGGGTGGTGGCATGCACCTGTATCTAGCTACTCGGAGGCTGAGGTGAGGGTA 2760
QY 2761 TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAAGCCATGACTGTGCCACTGTACTTCAGC 2820
DB 2761 TTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAAGCCATGACTGTGCCACTGTACTTCAGC 2820
QY 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGCTTAAAGT 2880
DB 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAGAGAGAGCTTAAAGT 2880
QY 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGGTAATTGGCAATGCCAT 2940
DB 2881 TGACTTTGTTCTTTATTTTAAATTTTATTTGGCTGAGCAGTGGGGTAATTGGCAATGCCAT 2940
QY 2941 TTCTGAGATGGTGAAGCCAGAGGAAGAGCAGTTTGGGGTAAATCAAGAGATCTGCATTTG 3000
DB 2941 TTCTGAGATGGTGAAGCCAGAGGAAGAGCAGTTTGGGGTAAATCAAGAGATCTGCATTTG 3000
QY 3001 GGACATGTTAAAGTTTGAGATTCCAGTCAAGGCTTCCAGTGGTGAAGCCACATAGGCAGTT 3060
DB 3001 GGACATGTTAAAGTTTGAGATTCCAGTCAAGGCTTCCAGTGGTGAAGCCACATAGGCAGTT 3060
QY 3061 CAGTGTGAAGAAATTCAGGACCAAGGCTGGGACGGTGGCTCCTCTGTCTAATCCAGCACT 3120
DB 3061 CAGTGTGAAGAAATTCAGGACCAAGGCTGGGACGGTGGCTCCTCTGTCTAATCCAGCACT 3120
QY 3121 TTGTTGCTGAGGACAGGTAGATCAATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCCAACA 3180
DB 3121 TTGTTGCTGAGGACAGGTAGATCAATTTGAGGTCAGGAGTTTGAGACAAGCTTGGCCCAACA 3180
QY 3181 TGGTGAACCCCATGCTACTAAAAATACAAAAATACAAAAATACAAAAATACAAAAATAC 3240
DB 3181 TGGTGAACCCCATGCTACTAAAAATACAAAAATACAAAAATACAAAAATACAAAAATAC 3240

QY 3241 ATAGTCCAGGCTTTTCAGGAGCTTAGGTAGGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
DB 3241 ATAGTCCAGGCTTTTCAGGAGCTTAGGTAGGAAATCCCTTGAACCCAGGAGGTGCAGG 3300
QY 3301 TTGCACTGAGCTGAGATTGTGCCACTGCACCTCCAGGCTGGGTGATAGAGTGAGACTCTGT 3360
DB 3301 TTGCACTGAGCTGAGATTGTGCCACTGCACCTCCAGGCTGGGTGATAGAGTGAGACTCTGT 3360
QY 3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420
DB 3361 CTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3420
QY 3421 TCTAATTTGCCCTGAGCACCACCTCCTGAGTTCACATGAGTGGCTAGACACACCTTAAC 3480
DB 3421 TCTAATTTGCCCTGAGCACCACCTCCTGAGTTCACATGAGTGGCTAGACACACCTTAAC 3480
QY 3481 ATTTCATAGATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGAT 3540
DB 3481 ATTTCATAGATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGAT 3540
QY 3541 CTGGGGCAGTGAAGGGTGGCAGCCACGTTGGCAGAGAAAAGCACACAGAAAGAGC 3600
DB 3541 CTGGGGCAGTGAAGGGTGGCAGCCACGTTGGCAGAGAAAAGCACACAGAAAGAGC 3600
QY 3601 ACCCAGGACTGTATATGGAAGAAAGACAGACTGCAACTCAACCTTCAAAAAATGAGGA 3660
DB 3601 ACCCAGGACTGTATATGGAAGAAAGACAGACTGCAACTCAACCTTCAAAAAATGAGGA 3660
QY 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
DB 3661 CCAGACACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3720
QY 3721 CTCTACTACACATGTTTAAAGCCCTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 3780
DB 3721 CTCTACTACACATGTTTAAAGCCCTGTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 3780
QY 3781 CTCTCTATGAGTGGCTCAGAGAGGACCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
DB 3781 CTCTCTATGAGTGGCTCAGAGAGGACCTTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3840
QY 3841 CGTGGATGACACAGCTTTCGTGTTCTATGATNATGAGATGCGCGTGTGGAGCCCGCAAC 3900
DB 3841 CGTGGATGACACAGCTTTCGTGTTCTATGATCATGAGATGCGCGTGTGGAGCCCGCAAC 3900
QY 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCTGACGCTGAGTCAGAGTCTGAA 3960
DB 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGCTGACGCTGAGTCAGAGTCTGAA 3960
QY 3961 AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAATAATCACACACAG 4020
DB 3961 AGGTTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGGAATAATCACACACAG 4020
QY 4021 CAAGGATGTGGAGAGGGGCCCTCACCTTCTCAGGTTGTGAGAGCTTTTTCATCTTTTC 4080
DB 4021 CAAGGATGTGGAGAGGGGCCCTCACCTTCTCAGGTTGTGAGAGCTTTTTCATCTTTTC 4080
QY 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 4140
DB 4081 ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGAGCAGGAGAGGGAAG 4140
QY 4141 GAATTTGCTCTCAGATCAATTTGGTCTGGGATGGTGGAAATAGGACCTATTCCTT 4200
DB 4141 GAATTTGCTCTCAGATCAATTTGGTCTGGGATGGTGGAAATAGGACCTATTCCTT 4200
QY 4201 TGGTTGCAAGTTAAACAGGCTGGGATTTTCCAGAGTCCACACCTGAGGCTCATCTG 4260
DB 4201 TGGTTGCAAGTTAAACAGGCTGGGATTTTCCAGAGTCCACACCTGAGGCTCATCTG 4260
QY 4261 GCGTGTGAATCCAGAGACACAGTACCAGGCGCTACTGGAAGTACGGGTATGATGGG 4320
DB 4261 GCGTGTGAATCCAGAGACACAGTACCAGGCGCTACTGGAAGTACGGGTATGATGGG 4320
QY 4321 CAGGACCACTTGAATTTCTGCCCTGACACACTGGAATGGAGAGCAGACAGACCCAGGCC 4380

|||||
Db 4321 CAGGACCACCTGAAATTCGCCCTGACACACTGGAATGGAGGACGACAGACCCAGGGCC 4380
QY 4381 TGGCCCAACAAGCTGGAGTGGGAAGGCAACAAGATTCGGGCCAGGCGAGCAAGAGGCCCTAC 4440
Db 4381 TGGCCCAACAAGCTGGAGTGGGAAGGCAACAAGATTCGGGCCAGGCGAGCAAGAGGCCCTAC 4440
QY 4441 CTGGAGAGGAGCTGCCCTGCACAGCTGCACAGCTGCTGGAGCTGGGAGAGGCTTTTGG 4500
Db 4441 CTGGAGAGGAGCTGCCCTGCACAGCTGCACAGCTGCTGGAGCTGGGAGAGGCTTTTGG 4500
QY 4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
Db 4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTTACTCTAGTGGCAGAGTGGAGG 4560
QY 4561 AGGTTGCAAGGACAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620
Db 4561 AGGTTGCAAGGACAGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC 4620
QY 4621 TCCAAATTCCTGGGAGGACTTCTCAATCCTAGAGTCTACCTTATATAGATGTA 4680
Db 4621 TCCAAATTCCTGGGAGGACTTCTCAATCCTAGAGTCTACCTTATATAGATGTA 4680
QY 4681 TGAGACGCCACAAGTCATGCGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAGGGAA 4740
Db 4681 TGAGACGCCACAAGTCATGCGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAGGGAA 4740
QY 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
Db 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
QY 4801 AAATTCAGAAATGCAAGCGCGGACGGTGGCTACCCCTGTATCCGAGCACTTTGGG 4860
Db 4801 AAATTCAGAAATGCAAGCGCGGACGGTGGCTACCCCTGTATCCGAGCACTTTGGG 4860
QY 4861 AGGCGGAGCGGGTGGTCACAAGGTCAGAGTTTGAGACCAGCTGACCAACATGGTAA 4920
Db 4861 AGGCGGAGCGGGTGGTCACAAGGTCAGAGTTTGAGACCAGCTGACCAACATGGTAA 4920
QY 4921 ACCGCTCTTAAANAATACANAATTTAGCTGGTCACAGTCATGGCACCTGTAGTCCA 4980
Db 4921 ACCGCTCTTAAANAATACANAATTTAGCTGGTCACAGTCATGGCACCTGTAGTCCA 4980
QY 4981 GCTAATTTGGAAGGCTGAGGCAAGGACATCGCTTGAACCTGGGAAGCGGAAGTTGCACATGA 5040
Db 4981 GCTAATTTGGAAGGCTGAGGCAAGGACATCGCTTGAACCTGGGAAGCGGAAGTTGCACATGA 5040
QY 5041 GCCAAGATCGGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA 5100
Db 5041 GCCAAGATCGGCCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAA 5100
QY 5101 AAAAAAANAANAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA 5160
Db 5101 AAAAAAANAANAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCAGGACAAA 5160
QY 5161 ATATCAAGTGAGGCACTTATCAGAGTAGAAGATCCTTTAGTTTAAAGTTTCTTTTCAT 5220
Db 5161 ATATCAAGTGAGGCACTTATCAGAGTAGAAGATCCTTTAGTTTAAAGTTTCTTTTCAT 5220
QY 5221 AGAATAGCAATATCTAGAGCTACCTATCTTTACAAGTCGGCTTCTTATAACAATGC 5280
Db 5221 AGAATAGCAATATCTAGAGCTACCTATCTTTACAAGTCGGCTTCTTATAACAATGC 5280
QY 5281 CTCCTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGGACATAA 5340
Db 5281 CTCCTAGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCATTTTCAATGGACATAA 5340
QY 5341 AGGGCAATTTATCTATCAGAACAAAGACATGGGTAAACAGATATGTATATTACATGTG 5400
Db 5341 AGGGCAATTTATCTATCAGAACAAAGACATGGGTAAACAGATATGTATATTACATGTG 5400
QY 5401 AGGAGAACAAAGCTGATCTGCTCTCCCAAGTGACACTGTGTAGAGTCCCAATCTTAGG 5460
|||||

Db 5401 AGGAGAACAAAGCTGATCTGACTGCTCTCCAAGTGACACTGTGTAGAGTCCCAATCTTAGG 5460
QY 5461 ACACAAAATGGTGCTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCTCTCTCTCC 5520
Db 5461 ACACAAAATGGTGCTCTCTCTGTAGCTTGTTTTTTCTGAAAAGGGTATTTCTCTCTCTCC 5520
QY 5521 AACCTATAGAAGGAAGTGAAGGTTCCAGTCTTCTGGCAAGGGTAAACAGATCCCTCTCTC 5580
Db 5521 AACCTATAGAAGGAAGTGAAGGTTCCAGTCTTCTGGCAAGGGTAAACAGATCCCTCTCTC 5580
QY 5581 CTCATCCTTCTCTCTCTCTCTCTCAAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACC 5640
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QY 5701 RAGTGGCTGAAGGATAAGCAGCCANTGGATGCCAAGAGTTTCGAACCTTAAAGAGTATTG 5760
Db 5701 RAGTGGCTGAAGGATAAGCAGCCANTGGATGCCAAGAGTTTCGAACCTTAAAGAGTATTG 5760
QY 5761 CCCAATGGGGATGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 5820
Db 5761 CCCAATGGGGATGGGACCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAG 5820
QY 5821 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGATCTGG 5880
Db 5821 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTGATCTGG 5880
QY 5881 GGTATGTGACTGTAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGGCC 5940
Db 5881 GGTATGTGACTGTAGAGCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGGCC 5940
QY 5941 TGAGAGGTAATATTGACAGTGAGATCTGCTCTTTTGTAGGGGTGGGCTGAGG 6000
Db 5941 TGAGAGGTAATATTGACAGTGAGATCTGCTCTTTTGTAGGGGTGGGCTGAGG 6000
QY 6001 GTGCAATCAAGGCTTTAACTTTCTGTTTTTACAGCCCTCACCCTCTGSCACCC 6060
Db 6001 GTGCAATCAAGGCTTTAACTTTCTGTTTTTACAGCCCTCACCCTCTGSCACCC 6060
QY 6061 TAGTCATTTGAGTCAATCAGTGGAAATGCTGTTTTTGTCTCATCTTTGTTCATTTGGAATTT 6120
Db 6061 TAGTCATTTGAGTCAATCAGTGGAAATGCTGTTTTTGTCTCATCTTTGTTCATTTGGAATTT 6120
QY 6121 TCTTCATAATATTAAAGAGAGGCAAGGTTCAAGTCAGTAGGAACAAGGGGGAAGTCTCT 6180
Db 6121 TCTTCATAATATTAAAGAGAGGCAAGGTTCAAGTCAGTAGGAACAAGGGGGAAGTCTCT 6180
QY 6181 TAGTACCTCTGCCCCAGGCAAGTGGGAAGAGGGGCAAGGGGATCTGGCATCCATGGG 6240
Db 6181 TAGTACCTCTGCCCCAGGCAAGTGGGAAGAGGGGCAAGGGGATCTGGCATCCATGGG 6240
QY 6241 AAGCAATTTTCTCATTTATATTCTTTGGGACACACAGAGCTCCCTGGGAGACAGAAAAAT 6300
Db 6241 AAGCAATTTTCTCATTTATATTCTTTGGGACACACAGAGCTCCCTGGGAGACAGAAAAAT 6300
QY 6301 AATGGTTCTCCCAAGATGAAAGTCTTAATCAAAAACATCTTTCAGAGCACCTACTAT 6360
Db 6301 AATGGTTCTCCCAAGATGAAAGTCTTAATCAAAAACATCTTTCAGAGCACCTACTAT 6360
QY 6361 TTTGCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
Db 6361 TTTGCAAGAGCTGTTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
QY 6421 TCTCAGAACCCAAATCTGGTAGGAAATGAAATGTAGCAAGTAAATGTAGTTAAAGAG 6480
Db 6421 TCTCAGAACCCAAATCTGGTAGGAAATGAAATGTAGCAAGTAAATGTAGTTAAAGAG 6480
QY 6481 ACCCATGAGTCTTAAAGCAGGCGAGGCAAAATCTTTAGGGTGTCAAAGGAAGAAATG 6540
Db 6481 ACCCATGAGTCTTAAAGCAGGCGAGGCAAAATCTTTAGGGTGTCAAAGGAAGAAATG 6540

Qy	6541	ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	6560
Db	6541	ATCNCATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTTGAAGGAGAAGCTGGATTCCA	6600
Qy	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGACGAGCAACCATGCCAAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTGAAGATGATGGAGGCTCTACACAGACGAGCAACCATGCCAAAGTAGGA	6660
Qy	6661	GAGTAAAGGCATACTGGAGATTAGAAATAATTACTGTACTTTACCCCTGAGTTTCGGT	6720
Db	6661	GAGTAAAGGCATACTGGAGATTAGAAATATTACTGTACTTTACCCCTGAGTTTCGGT	6720
Qy	6721	AGCTATCACTCACCAATATTATGCAATTTCTACCCCTGAACATCTGTGGGTGAGGAAAAGA	6780
Db	6721	AGCTATCACTCACCAATATTATGCAATTTCTACCCCTGAACATCTGTGGGTGAGGAAAAGA	6780
Qy	6781	GAATCAGAAAAGACCAAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAAGACCAAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTGGGTTATGA	6840
Qy	6841	TCAGTGGGCTGCAATGAAGGATCCCTAGAAGAGGAGCACCATCTCCCTTATATGGTG	6900
Db	6841	TCAGTGGGCTGCAATGAAGGATCCCTAGAAGAGGAGCACCATCTCCCTTATATGGTG	6900
Qy	6901	AATGTGTTGTTAAGAATTTAGATGAGAGGTGAGGAGCACCTAGTTAGAAAAGCCAAATAAGCAT	6960
Db	6901	AATGTGTTGTTAAGAATTTAGATGAGAGGTGAGGAGCACCTAGTTAGAAAAGCCAAATAAGCAT	6960
Qy	6961	TTCCAGATCAGAGATAATGGTCTCTTGAATCCAAATAGTGCCAGGCTCTAAATGAGATGG	7020
Db	6961	TTCCAGATCAGAGATAATGGTCTCTTGAATCCAAATAGTGCCAGGCTCTAAATGAGATGG	7020
Qy	7021	GTCAATGAGGAATAATAGGAAGAGAGAGGCGAGATGCTGCTAGTGTTCGTGATGCCT	7080
Db	7021	GTCAATGAGGAATAATAGGAAGAGAGAGGCGAGATGCTGCTAGTGTTCGTGATGCCT	7080
Qy	7081	CTTTCTGGGTCTCTTCTCCACAGAGAGAGCCNATGGGCACTACGCTTTAGCTGGAACG	7140
Db	7081	CTTTCTGGGTCTCTTCTCCACAGAGAGAGCCNATGGGCACTACGCTTTAGCTGGAACG	7140
Qy	7141	TGAGTGACACGACGCGCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAGA	7200
Db	7141	TGAGTGACACGACGCGCTGCAGACTCACTGTGGGAAGGAGACAAAACTAGAGACTCAAGA	7200
Qy	7201	GGGAGTGCAATTTATGAGCTCTCATCTTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
Db	7201	GGGAGTGCAATTTATGAGCTCTCATCTTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
Qy	7261	GCCTGACGAATCTTGATTTTAGCCTCTCTGTGTTCAATTTCTCTCAAAAAGATTTCCCAT	7320
Db	7261	GCCTGACGAATCTTGATTTTAGCCTCTCTGTGTTCAATTTCTCTCAAAAAGATTTCCCAT	7320
Qy	7321	TTAGGTTTCTGAGTTCTGCAATCCCGGTGATCCCTAGCTGTGACCTCTCCCTCGGAACGTG	7380
Db	7321	TTAGGTTTCTGAGTTCTGCAATCCCGGTGATCCCTAGCTGTGACCTCTCCCTCGGAACGTG	7380
Qy	7381	TCCTCATGACCTCAGCTGCAATCTAGAGGCTCTCTTCATTTCTTCCTCCGTACCTCAGAG	7440
Db	7381	TCCTCATGACCTCAGCTGCAATCTAGAGGCTCTCTTCATTTCTTCCTCCGTACCTCAGAG	7440
Qy	7441	ACATACACCTATGTCATTTCCATTTCCATTTTGGAGAGGACTCTCTAAATTTGGGGGA	7500
Db	7441	ACATACACCTATGTCATTTCCATTTCCATTTTGGAGAGGACTCTCTAAATTTGGGGGA	7500
Qy	7501	CTTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTTGGACAGCTGCTAGTCAT	7560
Db	7501	CTTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTTGGACAGCTGCTAGTCAT	7560
Qy	7561	AACCTTACAGATTTTACACATGTATCATGCATTTTCTGAGACCGGTTCAACTTTTCCT	7620
Db	7561	AACCTTACAGATTTTACACATGTATCATGCATTTTCTGAGACCGGTTCAACTTTTCCT	7620

Qy	7621	TTGAATCCCTCTCTCTGTGTTTACCCAGTA	CTACTCATCTGTCACCAAGCCTTGGGGATTCTTC	7680
Db	7621	TTGAATCCCTCTCTCTGTGTTTACCCAGTA	CTACTCATCTGTCACCAAGCCTTGGGGATTCTTC	7680
Qy	7681	CATCTGATTGTGATGTCGAGTTGACAGCTAT	GAAGGCTGTACACTGCACGAATGGAAGAG	7740
Db	7681	CATCTGATTGTGATGTCGAGTTGACAGCTAT	GAAGGCTGTACACTGCACGAATGGAAGAG	7740
Qy	7741	GCACCTGTCCACAGAAAAGCATCATGGCTAT	CTGTGGGTAGTATGATGGTCTTTTTAGC	7800
Db	7741	GCACCTGTCCACAGAAAAGCATCATGGCTAT	CTGTGGGTAGTATGATGGTCTTTTTAGC	7800
Qy	7801	AGSTAGGAGGCAATATCTTTGAAAGGGTGTG	GAAGAGGTGTTTTTCTTAATTGGCATGA	7860
Db	7801	AGSTAGGAGGCAATATCTTTGAAAGGGTGTG	GAAGAGGTGTTTTTCTTAATTGGCATGA	7860
Qy	7861	AGGTGTCATACAGATTTTGCAAGTTTAATG	SGTGCCCTCATTTGGGATGCTACTCTAGTAT	7920
Db	7861	AGGTGTCATACAGATTTTGCAAGTTTAATG	SGTGCCCTCATTTGGGATGCTACTCTAGTAT	7920
Qy	7921	TCCAGACCTTGAAGAATCACAAATAATTTCT	CTACTCGTCTCTCTGTTCTTGATAATGAAA	7980
Db	7921	TCCAGACCTTGAAGAATCACAAATAATTTCT	CTACTCGTCTCTCTGTTCTTGATAATGAAA	7980
Qy	7981	ATTATGATAAGATGATAAAGCAGCTTACTCT	CGTCTCGGACTCTCTGAGCAGCTACTTTA	8040
Db	7981	ATTATGATAAGATGATAAAGCAGCTTACTCT	CGTCTCGGACTCTCTGAGCAGCTACTTTA	8040
Qy	8041	CATGCAATTACTGCATGCAGCTCTTACAAATA	TTCTATGAGATAGTACTATTATCCCAT	8100
Db	8041	CATGCAATTACTGCATGCAGCTCTTACAAATA	TTCTATGAGATAGTACTATTATCCCAT	8100
Qy	8101	TTCTTTTTTAATGAAGAAAGTGAAGTGAAGT	AGGCGGCGACGGTGCTCACGCCGTGTAATCCC	8160
Db	8101	TTCTTTTTTAATGAAGAAAGTGAAGTGAAGT	AGGCGGCGACGGTGCTCACGCCGTGTAATCCC	8160
Qy	8161	AGCACTTTGGGAGGCCAAAGCGGGTGATCAG	AGGTCAGGAGATCGAGACCATCCTCGC	8220
Db	8161	AGCACTTTGGGAGGCCAAAGCGGGTGATCAG	AGGTCAGGAGATCGAGACCATCCTCGC	8220
Qy	8221	TAACATGSGTGAACCCCATCTCTTAATAAANA	TACAAAAATACAAAAATAGCTGGCGGTGGCAG	8280
Db	8221	TAACATGSGTGAACCCCATCTCTTAATAAANA	TACAAAAATACAAAAATAGCTGGCGGTGGCAG	8280
Qy	8281	ACGCCGTAGTCCCAAGCTACTCGGAAGGCTG	AGCAGGAGAAATGGCATGAACCCAGGAGG	8340
Db	8281	ACGCCGTAGTCCCAAGCTACTCGGAAGGCTG	AGCAGGAGAAATGGCATGAACCCAGGAGG	8340
Qy	8341	CAGAGCTTCGAGTGAGCGGAGTTTGGCCACT	GTGCACTCCAGCTTAGGTGACAGAGTGAGA	8400
Db	8341	CAGAGCTTCGAGTGAGCGGAGTTTGGCCACT	GTGCACTCCAGCTTAGGTGACAGAGTGAGA	8400
Qy	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATA	AAAAAATAAAAAAAGAAAGTGAAGTA	8460
Db	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATA	AAAAAATAAAAAAAGAAAGTGAAGTA	8460
Qy	8461	TAGATGATCTCATAGTTTGTCAGTGATAGAAA	ACGSGTTTCAAACTCAGTCAATCTGACCG	8520
Db	8461	TAGATGATCTCATAGTTTGTCAGTGATAGAAA	ACGSGTTTCAAACTCAGTCAATCTGACCG	8520
Qy	8521	TTTGATACATCTCAGACACCACTACATTCAGT	AGTTAGTAGTCCCTAGAAATAATAGAAA	8580
Db	8521	TTTGATACATCTCAGACACCACTACATTCAGT	AGTTAGTAGTCCCTAGAAATAATAGAAA	8580
Qy	8581	GGAAGAGAGATGGCTCTCTCTCTGTGTCAT	GTGTGTTTCTTCTGAGTGAGCTTGAATCACAT	8640
Db	8581	GGAAGAGAGATGGCTCTCTCTCTGTGTCAT	GTGTGTTTCTTCTGAGTGAGCTTGAATCACAT	8640
Qy	8641	GAGGGGAACACGAGAAAACCAACCACTGAT	CTCAGCTGTCATGTTTCCCTTTAAAGTCC	8700
Db	8641	GAGGGGAACACGAGAAAACCAACCACTGAT	CTCAGCTGTCATGTTTCCCTTTAAAGTCC	8700
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Db 8701 |||||CTGAAGGAAGGCTCTGAATGTGACTCCCTTCTCTCTGTTGCTCTCTTTGGCAATCA 8760
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REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Hereditary hemochromatosis gene products
JOURNAL Patent: US 6140305-A 3 31-Oct-2000;
FEATURES Location/Qualifiers
source 1..10825
BASE COUNT 2999 a 2953 c 2847 g 2926 t
ORIGIN

Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACCCCT 120
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Qy 121 TCAGGATTTAAACCAAGGGGACACTGGATCCTAGTCTTTCACAACGAGTACCTT 180
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Db	10261	TTTTTCTGGCTTTATTTCATAAAATCTTAAGGTCAACTACATTGAAAAATCAAGACCTG	10320
Qy	10321	CATTTTAAATTTCTATTCACTCTGCGAAACCAATTCACAAACCATGGTAGTAAGAGAA	10380
Db	10321	CATTTTAAATTTCTATTCACTCTGCGAAACCAATTCACAAACCAATGGTAGTAAGAGAA	10380
Qy	10381	GGGTGACACCTGGTGCCATAGTAAGTAATGATACACGGTGGTCCGGTGACCAAGATGCAG	10440
Db	10381	GGGTGACACCTGGTGCCATAGTAAGTAATGATACACGGTGGTCCGGTGACCAAGATGCAG	10440
Qy	10441	CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAGAAATGGGTGGAGGGCGTGCACTGGAA	10500
Db	10441	CGCTGAGGGTTTTCCTGAAGGTAAAGGAATAAGAAATGGGTGGAGGGCGTGCACTGGAA	10500
Qy	10501	ATCACCTGTAGAGAAAAGCCCTGAAAATTTGAGAAAACAAAAGAACTACTTACCAG	10560
Db	10501	ATCACCTGTAGAGAAAAGCCCTGAAAATTTGAGAAAACAAAAGAACTACTTACCAG	10560
Qy	10561	CTATTTGAATTTGCTGGAATCACAGGCCATTTGCTGAGCTGCCTGAACTGGGAACAACAG	10620
Db	10561	CTATTTGAATTTGCTGGAATCACAGGCCATTTGCTGAGCTGCCTGAACTGGGAACAACAG	10620
Qy	10621	AAGGAAAACAAACCACTCTGATAATCATGTAGTCAAGTACACAGCGTGAATGAGACTGC	10680
Db	10621	AAGGAAAACAAACCACTCTGATAATCATGTAGTCAAGTACACAGCGTGAATGAGACTGC	10680
Qy	10681	TCAGAGGTACAGGCCAAAATTTCTATGTTGTTATTAATAATGATCATCTTAATAFACGT	10740
Db	10681	TCAGAGGTACAGGCCAAAATTTCTATGTTGTTATTAATAATGATCATCTTAATAFACGT	10740
Qy	10741	CAGTATTTTATAAAACATTTCTCACAACCTCACACACATTTAAAAACAACACACTGTCTC	10800
Db	10741	CAGTATTTTATAAAACATTTCTCACAACCTCACACACATTTAAAAACAACACACTGTCTC	10800
Qy	10801	TAAATCCCAAAATTTTTCATAAAC	10825
Db	10801	TAAATCCCAAAATTTTTCATAAAC	10825
RESULT 4			
AR117792			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 10823; Conservative			
0; Mismatches			
2; Indels			
0; Gaps			
0;			
Qy	1	TCTRAGGTTGAGATAAAATTTTAAATGATGATTGATTTGAAATTCATAAATATTTA	60
Db	1	TCTRAGGTTGAGATAAAATTTTAAATGATGATTGATTTGAAATTCATAAATATTTA	60
Qy	61	AATATCTAAAGTTTCAGATCAGAACATTCGGAAGTACTTTCCCAATCAACACACCCCT	120
Db	61	AATATCTAAAGTTTCAGATCAGAACATTCGGAAGTACTTTCCCAATCAACACACCCCT	120

Qy	121	TCAGATTTAAAAACCAAGGGGACACTGGATCACTAGTCTTTTCAACAGCAGGTACCTT	180
Db	121	TCAGATTTAAAAACCAAGGGGACACTGGATCACTAGTCTTTTCAACAGCAGGTACCTT	180
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTACCAGGAAGTT	240
Db	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTACCAGGAAGTT	240
Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTACACTTCTGGAGCCATCCCG	300
Db	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTACACTTCTGGAGCCATCCCG	300
Qy	301	TTTCCCGCCGCCAAAAGAGCGGAGATTAAACGGGAGCTGCGGCCAGAGCTGGGAA	360
Db	301	TTTCCCGCCGCCAAAAGAGCGGAGATTAAACGGGAGCTGCGGCCAGAGCTGGGAA	360
Qy	361	ATGGGCCCGCGAGCAGCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGCTCTG	420
Db	361	ATGGGCCCGCGAGCAGCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGGCTCTG	420
Qy	421	CAGGGGCGCTTGTGCGTGAGTCCGAGGGCTGCGGGCGAACTAGGGCGCGGGGGTG	480
Db	421	CAGGGGCGCTTGTGCGTGAGTCCGAGGGCTGCGGGCGAACTAGGGCGCGGGGGTG	480
Qy	481	GAAAAATCGAAACTAGCTTTTCTTTCGCTTGGGAGTTTGCCTAACTTTGGAGGACCTGC	540
Db	481	GAAAAATCGAAACTAGCTTTTCTTTCGCTTGGGAGTTTGCCTAACTTTGGAGGACCTGC	540
Qy	541	TCAACCTATCCGCAAGCCCTCTCCCTACTTCTGCGTCCAGACCCCGTGAGGGAGTGC	600
Db	541	TCAACCTATCCGCAAGCCCTCTCCCTACTTCTGCGTCCAGACCCCGTGAGGGAGTGC	600
Qy	601	CTACCACTGAACATGACATAGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCGGGTGT	660
Db	601	CTACCACTGAACATGACATAGGGTCCCTCGCCCCAGGACCTGCCCCCTCCCCGGGTGT	660
Qy	661	CCGGCTCTCGGGAGTGACTTTTGGAAACCCCTCTCCCTTCCCTCCCACTAGAAATGCTTT	720
Db	661	CCGGCTCTCGGGAGTGACTTTTGGAAACCCCTCTCCCTTCCCTCCCACTAGAAATGCTTT	720
Qy	721	TAAATAATCTCGTAGTTCCTCACTTAGCTAGCTAAGCCTGGGGCTCCTTGAACCTGG	780
Db	721	TAAATAATCTCGTAGTTCCTCACTTAGCTAGCTAAGCCTGGGGCTCCTTGAACCTGG	780
Qy	781	AACTCGGGTTTATTTCCAATGTCAGCTGTCAGCTTTTCCCGCAGTCATCTCAAACAGG	840
Db	781	AACTCGGGTTTATTTCCAATGTCAGCTGTCAGCTTTTCCCGCAGTCATCTCAAACAGG	840
Qy	841	AAGTTCTTCCTCAGTGTCTTCCGAGAAAGCTGAGCAAAACCCACAGAGATCCGCACGG	900
Db	841	AAGTTCTTCCTCAGTGTCTTCCGAGAAAGCTGAGCAAAACCCACAGAGATCCGCACGG	900
Qy	901	GGTTTCCACCTCAGAACGAATGCGTTGGGGGTGGGGCGCGGAAAGAGTGGGCTGGGA	960
Db	901	GGTTTCCACCTCAGAACGAATGCGTTGGGGGTGGGGCGCGGAAAGAGTGGGCTGGGA	960
Qy	961	TCTGAATTTCTTCAACATTCACCCACTTTTGGTGACCTGGGGTGGAGTCTCTAGGCT	1020
Db	961	TCTGAATTTCTTCAACATTCACCCACTTTTGGTGACCTGGGGTGGAGTCTCTAGGCT	1020
Qy	1021	GGAGGCTCCTGAGAGAGCCCTACCTCGGGCTTTTCCCGCACTTTGGCAATTTGCTTTT	1080
Db	1021	GGAGGCTCCTGAGAGAGCCCTACCTCGGGCTTTTCCCGCACTTTGGCAATTTGCTTTT	1080
Qy	1081	GCCTGAAATTAAGTATATGTTAGTTTGAAGCTTTGAACGTTGAACGAACTCTCTTCGG	1140
Db	1081	GCCTGAAATTAAGTATATGTTAGTTTGAAGCTTTGAACGTTGAACGAACTCTCTTCGG	1140
Qy	1141	CTAGGCTTTATTGATTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAGTACTGA	1200
Db	1141	CTAGGCTTTATTGATTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAGTACTGA	1200

QY 1201 TAATGAACATGTAAGCAATGCACCTCACTTCTAAGTTACATATCATATCTGATCTTATTTGA 1260
DB 1201 TAATGAACATGTAAGCAATGCACCTCACTTCTAAGTTACATATCATATCTGATCTTATTTGA 1260
QY 1261 TTTTCTACTAGGCATAGGGAGGTAGGAGCTAAATAATACGTTTATTTTACTAGAACTAACT 1320
DB 1261 TTTTCTACTAGGCATAGGGAGGTAGGAGCTAAATAATACGTTTATTTTACTAGAACTAACT 1320
QY 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGACATAAATAATCTGTTTCTTG 1380
DB 1321 GGAATTCAGATTAATAAATCTTTTTCAGGTTACAAAGACATAAATAATCTGTTTCTTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTAGACAGTATTTTGCCCTGTAG 1440
DB 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTAGACAGTATTTTGCCCTGTAG 1440
QY 1441 TGTAGCACAGTGTCTGTGGGTACAGCGCGGCTCAGCACAGCATTTGAGTTTGGTA 1500
DB 1441 TGTAGCACAGTGTCTGTGGGTACAGCGCGGCTCAGCACAGCATTTGAGTTTGGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCGCTGCTTCTGTG 1560
DB 1501 CTACGTGTATCCACATTTTACACATGACAAGATGAGGCATGGCAGCGCTGCTTCTGTG 1560
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DB 1561 CAAATTTTAAATGTPACACTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTTAAACATCACACTGCATTTAGAGGTTGAATAATAAATTTTATGTTGAGCAG 1680
DB 1621 TATGATTTTAAACATCACACTGCATTTAGAGGTTGAATAATAAATTTTATGTTGAGCAG 1680
QY 1681 AAATATTCATTTTACAAGTGAATAGTCCAGCCATGTGTGACACTGTGTTCAAGCCC 1740
DB 1681 AAATATTCATTTTACAAGTGAATAGTCCAGCCATGTGTGACACTGTGTTCAAGCCC 1740
QY 1741 CAAGGGAGAGCAGGGAACAAGTCTTTACCCCTTTCATATTTTGCATCTAGTGGGAGA 1800
DB 1741 CAAGGGAGAGCAGGGAACAAGTCTTTACCCCTTTCATATTTTGCATCTAGTGGGAGA 1800
QY 1801 GATGACAAATAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGTGTGTGA 1860
DB 1801 GATGACAAATAGCAAAATGAGCAGAAAGATATACAACATCAGGAAATCATGGTGTGTGA 1860
QY 1861 GAAGCAGAGAAGTCAGGCAAGTCACCTCTGGGCTGACACTTTGAGCAGACATGAAGGA 1920
DB 1861 GAAGCAGAGAAGTCAGGCAAGTCACCTCTGGGCTGACACTTTGAGCAGACATGAAGGA 1920
QY 1921 AATAAGATGATATTGACTGGGAGCAGTATTTCCAGCAAACTGAGTGGGCCCTGGCAAG 1980
DB 1921 AATAAGATGATATTGACTGGGAGCAGTATTTCCAGCAAACTGAGTGGGCCCTGGCAAG 1980
QY 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
DB 1981 TTGGATTTAAAGCGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATCTTAGCAGTATCTCTGT 2100
DB 2041 CGGCGTGGGGTGGGAAGGGGACTACCATCTGCATGTAGGATCTTAGCAGTATCTCTGT 2100
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DB 2101 CCTCCCTACTCACTAGGTGCTAGGAGCACTCCCCAGTCTTTGACAAACAAATGCTCTCT 2160
QY 2161 AAATTTTCCACATGTCACCTAGTAGACAACTCTCTGGTTTAAAGAGCTCGGGTTGAAAAA 2220
DB 2161 AAATTTTCCACATGTCACCTAGTAGACAACTCTCTGGTTTAAAGAGCTCGGGTTGAAAAA 2220
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DB 2221 AATAACAGTAGTCTGGGAGTAGAGCCCAAGAGTAGGTAAATGGGCTCAGAGAGGA 2280
QY 2281 GCCACAAACAAGGTTGTGCGCGGCTGTAGGCTGTGCTGTAATTTCTAGCCAAAGGAGTA 2340

DB 2281 GCCACAAACAAGGTTGTGCGCGGCTGTAGGCTGTGCTGTAATTTAGCCAAAGGAGTA 2340
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DB 2341 ACAGTGATCTGTGCAGAGCTTTTAAAGATTGCTCTGGCTGCTATGTGGAAGCAGAAATG 2400
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DB 2401 AAGGAGCAACAGTAAAAAGCAGGAGCCAGCCAGGAAAGTGTACACAGTCCAGGCAAG 2460
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DB 2461 AGGTAGTGGAGTGGCTGGGTGGGAACAGAAAGGAGTGACAACCAATTTCTCTCTGAA 2520
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DB 2521 TATATTTCTGAAGAAATTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAANAATTTG 2580
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DB 2581 CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGAGCAGATTTCTGAGCTCAGGA 2640
QY 2641 GTTCAGACCAACCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
DB 2641 GTTCAGACCAACCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
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DB 2701 GCTGGTGTGGTGGCATGCACCTGTCTAGCTACTCGGGAGGCTGAGTGGAGGTA 2760
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DB 2821 CTAGGTGACAGAGCAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAGAGTTAAAGT 2880
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DB 2881 TGACTTTGTTCTTTTATTTTATTTTATTTGCGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
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DB 2941 TTCTGAGATGGTGAAGCAGAGAGAAAGACAGTTTGGGTAATCAAGGATCTGCATTTG 3000
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DB 3061 CAGTGTAAAGATTCAGGACCAAGGCTGGCAGCGTGGCTCACTTCTGTAATCCCAGCACT 3120
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QY 3181 TGTGAAACCCCATGTCTACTAAAAATACAAAATTTAGGCTGGTGGTGCGCAGGCT 3240
DB 3181 TGTGAAACCCCATGTCTACTAAAAATTTAGGCTGGTGGTGCGCAGGCT 3240
QY 3241 ATAGTCCCAGGTTTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGAGTGCAGG 3300
DB 3241 ATAGTCCCAGGTTTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGAGTGCAGG 3300
QY 3301 TTGCACTGAGCTGAGATTTGTCACCTGCACCTCCAGGCTGGGTGATAGAGTGCAGCTCTGT 3360
DB 3301 TTGCACTGAGCTGAGATTTGTCACCTGCACCTCCAGGCTGGGTGATAGAGTGCAGCTCTGT 3360
QY 3361 CTCAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 3420

Db 3361 CTCAAAAA...TTTCTCCTCAGGATTGGG 3420
 Qy 3421 TCTAAATGGCCGTGAGCACCACCTCCTGAGTTCACATACCATGGCTAGACACACCTTAAC 3480
 Db 3421 TCTAAATGGCCGTGAGCACCACCTCCTGAGTTCACATACCATGGCTAGACACACCTTAAC 3480
 Qy 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAAATCATGAGTATTGGAATAGGAT 3540
 Db 3481 ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAAATCATGAGTATTGGAATAGGAT 3540
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 Db 3541 CTGGGGGAGTGGAGGGGTGGAGCCAGCTGTGGCAGAGAAAGCACACAGGAAGAGAGC 3600
 Qy 3601 ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCACAAAAATGAGGA 3660
 Db 3601 ACCCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCACAAAAATGAGGA 3660
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 Db 3661 CCAGACACAGCTGATGGTATGAGTTGATGCGAGGTGTGTGGAGCCTCAACATCTGCTCCC 3720
 Qy 3721 CTCCTACTACACATGGTTAAGCCCTGTTGCTCTGTCTCCAGGTTTCACACACTCTGCACTA 3780
 Db 3721 CTCCTACTACACATGGTTAAGCCCTGTTGCTCTGTCTCCAGGTTTCACACACTCTGCACTA 3780
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 Db 3781 CCTCTTCATGGGTGCTCAGACAGGACCTTGGTCTTCTTCTTGTGAACTTTGGGCTA 3840
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 Db 3901 TCCATGGGTTCCAGTAGAAATTCAGCCAGATGTGGCTGCAGCTGAGTTCAGAGTCTGAA 3960
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 Db 3961 AGGTTGGATCATCATGTTTCACTGTTGACTTCTGCACTATATGAAAAATCACAACACAG 4020
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 Db 4021 CARAGGTATGTGAGAGGGGCTCACCTTCCTGAGGTGTCAGAGCTTTTCATCTTTTC 4080
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 Db 5461 ACACAAATGGTCTCTCTCTCTAGCTTTTCTGAAAAAGGATTTTCTTCTCTCC 5520
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 Db 5521 AACCTATAGAGGAAGTGAAGTTCAGTCTTCTGGCAAGGGTAAACAGATCCCTCTCT 5580

Qy	5581	CTCATCTCTCTCTTCCCTGTC	CAAGTGCCTCCTTTTGTG	GAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTCTCTCTTCCCTGTC	CAAGTGCCTCCTTTTGTG	GAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTTCAGTGAACCACTCT	ACGGTGTGCGGCCCTTG	GAACCTACTACCCCCAGAACATCACCATTG	5700
Db	5641	TCCTTCAGTGACCACTCT	ACGGTGTGCGGCCCTTG	GAACCTACTACCCCCAGAACATCACCATTG	5700
Qy	5701	AACTGGCTGAAGGATGAAG	CAGCAATGATGCCAAG	AGGTTCGAACCTAAAGACGATATG	5760
Db	5701	AACTGGCTGAAGGATGAAG	CAGCAATGATGCCAAG	AGGTTCGAACCTAAAGACGATATG	5760
Qy	5761	CCCAATGGGATGGGACCT	TACCAGGCTGAGATTA	ACCTTGGCTGACCCCTGGGGAAGAG	5820
Db	5761	CCCAATGGGATGGGACCT	TACCAGGCTGAGATTA	ACCTTGGCTGACCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATACGPNCCAG	TGAGCACCAGCCCTGG	ATCAGCCCTCATTTGATCTGG	5880
Db	5821	CAGAGATATACGPNCCAG	TGAGCACCAGCCCTGG	ATCAGCCCTCATTTGATCTGG	5880
Qy	5881	GGTATGTGACTGATGAG	AGCCAGGCTCAGAAA	ATCTATTGGGGTGTGAGAGAGTGCC	5940
Db	5881	GGTATGTGACTGATGAG	AGCCAGGCTCAGAAA	ATCTATTGGGGTGTGAGAGAGTGCC	5940
Qy	5941	TGAGGAGGTAATTTAT	GGCAGTGAAGATCTG	CTCTTTTGGGGTGGGCTGAGG	6000
Db	5941	TGAGGAGGTAATTTAT	GGCAGTGAAGATCTG	CTCTTTTGGGGTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAGGCTTT	TAACCTGCTTTTCTG	TTTATAGAGCCCTCACCGTCTGGCACCC	6060
Db	6001	GTGGCAATCAAGGCTTT	TAACCTGCTTTTCTG	TTTATAGAGCCCTCACCGTCTGGCACCC	6060
Qy	6061	TAGTCATTTGAGTGCAT	AGTGAATGCTGTTT	TGTCGTCATCTGTTTCATTTGGAATTT	6120
Db	6061	TAGTCATTTGAGTGCAT	AGTGAATGCTGTTT	TGTCGTCATCTGTTTCATTTGGAATTT	6120
Qy	6121	TGTTTCATTAATTAAG	GAAGAGGAGGTTC	CAAGTGAAGTGAAGCAAGGGGAGTCTCT	6180
Db	6121	TGTTTCATTAATTAAG	GAAGAGGAGGTTC	CAAGTGAAGTGAAGCAAGGGGAGTCTCT	6180
Qy	6181	TAGTACCTTCGCCAGG	GCACAGTGGGAAG	GGGCAAGGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACCTTCGCCAGG	GCACAGTGGGAAG	GGGCAAGGGGATCTGGCATCCATGGG	6240
Qy	6241	AAGCATTTTCTCATTT	ATATATCTTTTGGG	GACACCCAGCAGCTCCCTGGGAGACAGAAAAT	6300
Db	6241	AAGCATTTTCTCATTT	ATATATCTTTTGGG	GACACCCAGCAGCTCCCTGGGAGACAGAAAAT	6300
Qy	6301	AATGGTTCCTCCAGAA	TGAAAGTCTCTAAT	TTCAACAACATCTTCAGAGCACCCTACTAT	6360
Db	6301	AATGGTTCCTCCAGAA	TGAAAGTCTCTAAT	TTCAACAACATCTTCAGAGCACCCTACTAT	6360
Qy	6361	TTTSCAAGAGCTCTTT	TAAGGTAGTACAGG	GGCTTTTGAAGTTGAGAAGTCACTGTGGCTAT	6420
Db	6361	TTTSCAAGAGCTCTTT	TAAGGTAGTACAGG	GGCTTTTGAAGTTGAGAAGTCACTGTGGCTAT	6420
Qy	6421	TCTCAGAACCCAAAT	CTGGTAGGAATGAAT	TGTATAGCAAGTAAATGTAGTTAAAGAAG	6480
Db	6421	TCTCAGAACCCAAAT	CTGGTAGGAATGAAT	TGTATAGCAAGTAAATGTAGTTAAAGAAG	6480
Qy	6481	ACCCATGAGGTCCTTA	AGCAGCAGGAACAA	TGCTTAGGGTGTCAAGGAAGAAGATG	6540
Db	6481	ACCCATGAGGTCCTTA	AGCAGCAGGAACAA	TGCTTAGGGTGTCAAGGAAGAAGATG	6540
Qy	6541	ATCACATTCAGCTGGG	ATCAAGATAGCCTT	CTGGAATCTTGAAGGAGAGCTGGATTCCA	6600
Db	6541	ATCACATTCAGCTGGG	ATCAAGATAGCCTT	CTGGAATCTTGAAGGAGAGCTGGATTCCA	6600
Qy	6601	TTAGGTGAGGTTCA	AGATGATGGAGGTC	TACACAGCAGCAACCATGCTCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTCA	AGATGATGGAGGTC	TACACAGCAGCAACCATGCTCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCAT	TACTGGGAGATTA	GAAAATAATTACTGTACCTTAACCCCTGAGTTTCGCT	6720
Db	6661	GAGTATAAGGCAT	TACTGGGAGATTA	GAAAATAATTACTGTACCTTAACCCCTGAGTTTCGCT	6720
Qy	6721	AGCTATCACATCACA	ATATATGCAATTTCT	ACCCCTGAACATCTGTGTAGGGAAGAAGA	6780
Db	6721	AGCTATCACATCACA	ATATATGCAATTTCT	ACCCCTGAACATCTGTGTAGGGAAGAAGA	6780
Qy	6781	GAATCAGAAAAGAG	CCAGCTCATACAGAG	TCCCAAGGGCTTTTGGGATATATGGGTTATGA	6840
Db	6781	GAATCAGAAAAGAG	CCAGCTCATACAGAG	TCCCAAGGGCTTTTGGGATATATGGGTTATGA	6840
Qy	6841	TCACCTGGGTGTCT	ATTTGAAGGATCC	TAAAGAGAGGACCATCTCCCTTATATGGTG	6900
Db	6841	TCACCTGGGTGTCT	ATTTGAAGGATCC	TAAAGAGAGGACCATCTCCCTTATATGGTG	6900
Qy	6901	AATGTGTTTAAAGAT	TAGATGAGAGGT	TAGAGGACCATTTAGAAAAGCCCAATAAGCAT	6960
Db	6901	AATGTGTTTAAAGAT	TAGATGAGAGGT	TAGAGGACCATTTAGAAAAGCCCAATAAGCAT	6960
Qy	6961	TTCCAGATGAGAGAT	AATGGTCTTGAAT	TCCAATCCAATAGTGCCAGGCTCAATTTGAGATGG	7020
Db	6961	TTCCAGATGAGAGAT	AATGGTCTTGAAT	TCCAATCCAATAGTGCCAGGCTCAATTTGAGATGG	7020
Qy	7021	GTGAATGAGGAAAT	TAGAGAGGAC	AGGCAAGATGGTGCCTAGGTTTGTGATGCCT	7080
Db	7021	GTGAATGAGGAAAT	TAGAGAGGAC	AGGCAAGATGGTGCCTAGGTTTGTGATGCCT	7080
Qy	7081	CTTTCTCTGGGTCT	CTCTCCACAGAG	AGCCATGGGGCCTACGTCCTTAGCTGAACG	7140
Db	7081	CTTTCTCTGGGTCT	CTCTCCACAGAG	AGCCATGGGGCCTACGTCCTTAGCTGAACG	7140
Qy	7141	TGAGTGACAGCGAG	CCCTGCAGACT	CACTGTGGAGAGGACAAAACCTAGAGACTCAAGA	7200
Db	7141	TGAGTGACAGCGAG	CCCTGCAGACT	CACTGTGGAGAGGACAAAACCTAGAGACTCAAGA	7200
Qy	7201	GGGAGTGCAATTT	ATGAGCTCTTCAT	GTTCAGSAGAGAGTTGAACTTAAACATAGAAAT	7260
Db	7201	GGGAGTGCAATTT	ATGAGCTCTTCAT	GTTCAGSAGAGAGTTGAACTTAAACATAGAAAT	7260
Qy	7261	GCCTGACGAACCT	CTTGATTTAGCCT	CTCTGTCATTTCCCTGAAAAGATTTCCCCAT	7320
Db	7261	GCCTGACGAACCT	CTTGATTTAGCCT	CTCTGTCATTTCCCTGAAAAGATTTCCCCAT	7320
Qy	7321	TTAGGTTTCTGAGT	TCCTGATCCCGT	GATCCCTAGCTGTGACCTCTCCCTGGAATG	7380
Db	7321	TTAGGTTTCTGAGT	TCCTGATCCCGT	GATCCCTAGCTGTGACCTCTCCCTGGAATG	7380
Qy	7381	TCTCTCATGAACCT	CAAGCTGCATCT	AGAGGCTTCCCTCATTTCCCTGACCTCAGAG	7440
Db	7381	TCTCTCATGAACCT	CAAGCTGCATCT	AGAGGCTTCCCTCATTTCCCTGACCTCAGAG	7440
Qy	7441	ACATACACCTAT	GTGTCATTTTCC	TATTTTGGAGAGGACTCCTTTAAATTTGGGGGA	7500
Db	7441	ACATACACCTAT	GTGTCATTTTCC	TATTTTGGAGAGGACTCCTTTAAATTTGGGGGA	7500
Qy	7501	CTTACATGATTCAT	TTTAAACATCTG	AGAAAAGCTTTGAACCCCTGGAGCTGGCTAGTCAT	7560
Db	7501	CTTACATGATTCAT	TTTAAACATCTG	AGAAAAGCTTTGAACCCCTGGAGCTGGCTAGTCAT	7560
Qy	7561	AACCTTACCAGAT	TTTTACACATGT	ATCTATGCAATTTTCTGGACCCCTTCAACTTTTCCCT	7620
Db	7561	AACCTTACCAGAT	TTTTACACATGT	ATCTATGCAATTTTCTGGACCCCTTCAACTTTTCCCT	7620
Qy	7621	TTGAATCCTCTCT	CTGTGTTACCC	AGTAACCTCATCTGTGCACCAAGCTTTGGGATCTTTC	7680
Db	7621	TTGAATCCTCTCT	CTGTGTTACCC	AGTAACCTCATCTGTGCACCAAGCTTTGGGATCTTTC	7680
Qy	7681	CATCTGATTTGT	GATGTGAGTTG	CACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG	7740
Db	7681	CATCTGATTTGT	GATGTGAGTTG	CACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG	7740
Qy	7741	GCACCTGTCC	CAGAAAAGCAT	CATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTACG	7800
Db	7741	GCACCTGTCC	CAGAAAAGCAT	CATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTACG	7800

Db 7741 GCACCTGTCGCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGGTGTTTTFAGC 7800
Qy 7801 AGGTAGGAGCAATATCTTTGAAAGGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA 7860
Db 7801 AGGTAGGAGCAATATCTTTGAAAGGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA 7860
Qy 7861 AGGTGTCATACAGATTGGCAAGTTTAATGGTGCCTTCATTTGGGATCCTACTCTAGTAT 7920
Db 7861 AGGTGTCATACAGATTGGCAAGTTTAATGGTGCCTTCATTTGGGATCCTACTCTAGTAT 7920
Qy 7921 TCCAGACCTGAGAAATCACAATAATTTCTACCTGCTCTCTCTCTGTTCTGATAATGAAA 7980
Db 7921 TCCAGACCTGAGAAATCACAATAATTTCTACCTGCTCTCTCTCTGTTCTGATAATGAAA 7980
Qy 7981 ATTATGATAAGGATGATAAAGACCTTACTTCGTGTCGGACTTCTCTGAGCACCTACTFTA 8040
Db 7981 ATTATGATAAGGATGATAAAGACCTTACTTCGTGTCGGACTTCTCTGAGCACCTACTFTA 8040
Qy 8041 CATGCATTTACTGCATGCATCTCTTACAATAATTTCTATGAGATAGTACTATTATCCCAT 8100
Db 8041 CATGCATTTACTGCATGCATCTCTTACAATAATTTCTATGAGATAGTACTATTATCCCAT 8100
Qy 8101 TTCTTTTAAAGAAAGTGAAGTAGGCGGGCAGGTGGCTACGCCCTGTAATCCC 8160
Db 8101 TTCTTTTAAAGAAAGTGAAGTAGGCGGGCAGGTGGCTACGCCCTGTAATCCC 8160
Qy 8161 AGCACTTTGGGAGCCAAAGCGGTGGATCACGAGTTCAGAGATCGAGACCATCTCGC 8220
Db 8161 AGCACTTTGGGAGCCAAAGCGGTGGATCACGAGTTCAGAGATCGAGACCATCTCGC 8220
Qy 8221 TAACATGGTGAACCCCATCTCTTAATAAATAACAAAAATTTAGCTGGCGGTGGTGGCAG 8280
Db 8221 TAACATGGTGAACCCCATCTCTTAATAAATAACAAAAATTTAGCTGGCGGTGGTGGCAG 8280
Qy 8281 ACGCCTGTAGTCCAGCTACTCGGAAGCTGAGGAGGATGCGATGCAACCCAGGAGG 8340
Db 8281 ACGCCTGTAGTCCAGCTACTCGGAAGCTGAGGAGGATGCGATGCAACCCAGGAGG 8340
Qy 8341 CAGAGCTTGCAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCTAGGTGACAGAGTGAGA 8400
Db 8341 CAGAGCTTGCAGTGAGCCGAGTTTGGCCACTGCACCTCCAGCTAGGTGACAGAGTGAGA 8400
Qy 8401 CTCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8460
Db 8401 CTCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 8460
Qy 8461 TAGAGTATCTCATAGTTTGTGCTGATGAAACAGGTTTCAACACTCAGTCAATCTGACCG 8520
Db 8461 TAGAGTATCTCATAGTTTGTGCTGATGAAACAGGTTTCAACACTCAGTCAATCTGACCG 8520
Qy 8521 TTTGATACATCTCAGACACCTACATTCAGTAGTTAGATGCCCTAGATAAATAAGAGAA 8580
Db 8521 TTTGATACATCTCAGACACCTACATTCAGTAGTTAGATGCCCTAGATAAATAAGAGAA 8580
Qy 8581 GGAAGGATGGCTCTCTCTGCTCATTTGTTCTGCTGAGTGAGCTTGAATCACAT 8640
Db 8581 GGAAGGATGGCTCTCTCTGCTCATTTGTTCTGCTGAGTGAGCTTGAATCACAT 8640
Qy 8641 GAAGGGACAGCAGAAAAACCAACTGATCCTCAGCTGTGATGTTTCCCTTTAAAAAGTC 8700
Db 8641 GAAGGGACAGCAGAAAAACCAACTGATCCTCAGCTGTGATGTTTCCCTTTAAAAAGTC 8700
Qy 8701 CCTGAAGGAGTCCCTGGATGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8760
Db 8701 CCTGAAGGAGTCCCTGGATGACTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 8760
Qy 8761 TTTCTTTGGACCTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
Db 8761 TTTCTTTGGACCTACGCAAGGACTGTAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC 8820
Qy 8821 TTCACACACCGGTGCTCCCTAGGCCAGTGCCTCTGGAGTCAAGACTCTGGTGGTATTTC 8880
Db 8821 TTCACACACCGGTGCTCCCTAGGCCAGTGCCTCTGGAGTCAAGACTCTGGTGGTATTTC 8880

Qy 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCAATTTGAGATGATGATGATGATGATGATGATGATG 8940
Db 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCAATTTGAGATGATGATGATGATGATGATGATGATG 8940
Qy 8941 GCTTAGAGATGCCAGGTCCTTCCATGAGCACTGCGGTCCGGTCCGATCAATAAAAA 9000
Db 8941 GCTTAGAGATGCCAGGTCCTTCCATGAGCACTGCGGTCCGGTCCGATCAATAAAAA 9000
Qy 9001 AAAATCAACAGGACATTCAGGAATTTGCTAGATTTCTGGAAATCAGTTCCACCATGTTCA 9060
Db 9001 AAAATCAACAGGACATTCAGGAATTTGCTAGATTTCTGGAAATCAGTTCCACCATGTTCA 9060
Qy 9061 AAAGAGCTTT 9120
Db 9061 AAAGAGCTTT 9120
Qy 9121 CTCGGCTCACTGTAACCTCTGCTCCAGGTTCAAGCACTCTCCTGACCTCGTATGATGATG 9180
Db 9121 CTCGGCTCACTGTAACCTCTGCTCCAGGTTCAAGCACTCTCCTGACCTCGTATGATGATG 9180
Qy 9181 AGTAGCTGGATTTACAGGCGTGCACCACTGCTCCGGCTAAATTTTGTATTTTAGTAGTA 9240
Db 9181 AGTAGCTGGATTTACAGGCGTGCACCACTGCTCCGGCTAAATTTTGTATTTTAGTAGTA 9240
Qy 9241 GACAGGTTTTCACATGTTGGCCAGGCTGCTCGAACTCTCCTGACCTCGTATGATGATG 9300
Db 9241 GACAGGTTTTCACATGTTGGCCAGGCTGCTCGAACTCTCCTGACCTCGTATGATGATG 9300
Qy 9301 TGCCCTCGGCTCCCAAGTGTGAGATTTACAGGTGTGAGCCACCCTGCCAGCGGTCAAA 9360
Db 9301 TGCCCTCGGCTCCCAAGTGTGAGATTTACAGGTGTGAGCCACCCTGCCAGCGGTCAAA 9360
Qy 9361 AGAGTCTTAATATATATATCCAGATGSCATGTTTACTTTTACTTTACTTACTTACTTACTT 9420
Db 9361 AGAGTCTTAATATATATATCCAGATGSCATGTTTACTTTTACTTTACTTACTTACTTACTT 9420
Qy 9421 GCTGCATAAATGTGTACAGCAATCTGCTTTGAAGGCGAGGTGCTTCAGGATACCATAT 9480
Db 9421 GCTGCATAAATGTGTACAGCAATCTGCTTTGAAGGCGAGGTGCTTCAGGATACCATAT 9480
Qy 9481 ACAGCTCAGAAAGTTCTCTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9540
Db 9481 ACAGCTCAGAAAGTTCTCTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9540
Qy 9541 TTAACCACTTTCTTTTTTTTGTGTTAGAAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Db 9541 TTAACCACTTTCTTTTTTTTGTGTTAGAAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Qy 9601 ACAGCTCAGAAAGTTCTCTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9660
Db 9601 ACAGCTCAGAAAGTTCTCTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9660
Qy 9661 TGAACCACTTTAACAACCTTTCTATTACCTGTTAGTATTTAGTATTTAGTATTTAGTATTT 9720
Db 9661 TGAACCACTTTAACAACCTTTCTATTACCTGTTAGTATTTAGTATTTAGTATTTAGTATTT 9720
Qy 9721 TATACCTTAATAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9780
Db 9721 TATACCTTAATAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 9780
Qy 9781 ATCTGTGATATATCTTAATTCGCTTTGTCATTTTGGAGACATTTATTTTGGTCTTAATTT 9840
Db 9781 ATCTGTGATATATCTTAATTCGCTTTGTCATTTTGGAGACATTTATTTTGGTCTTAATTT 9840
Qy 9841 CTTTACATTTTGTCTTACGGAATTTTTCATTAACCTGTTGGTGGGCAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGTCTTACGGAATTTTTCATTAACCTGTTGGTGGGCAATTAATCGTGT 9900
Qy 9901 TCTTCACTCTAGGACATGCTGCTCAAGTGTGAGACATTTGTTATTTTACCAGCAAC 9960
Db 9901 TCTTCACTCTAGGACATGCTGCTCAAGTGTGAGACATTTGTTATTTTACCAGCAAC 9960

Qy	3061	CAGTGTGAAGAAATTCAGGACCAAGCGTGGCCACGCTGGCTCACCTCTGTATATCCACGACACT	3120
Db	3061		
Qy	3121	TTGGTGGCTGAGGCAGGTAGATCATTTTCAGCTCAGGAGTTTGAGACAAGCTTGGCCACA	3180
Db	3121		
Qy	3181	TGGTGAACCCCATGTCTACTAAAAATACAAAAATAGCCCTGGTGTGGTGGCGACGCGCT	3240
Db	3181		
Qy	3241	ATAGTCCCGAGTTTTCAGGAGCGTTAGTGTAGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
Db	3241		
Qy	3301	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301		
Qy	3361	CTCAAAAAAATAAAAAAAAAAAAAAAAAAACAATGAGGAATATTTCCTCAGGATTGGG	3420
Db	3361		
Qy	3421	TCTAAATTTGCCCTGAGCACCAACTCCTCAGTTCAACTACCATGGCTAGACACACCTTTAAC	3480
Db	3421		
Qy	3481	ATTTTCTAGAAATCCACACGCTTTAGTGGAGTCTGTCTTAATCATCAGTATTGGGAATAGGAT	3540
Db	3481		
Qy	3541	CTGGGGCAGTGAGGGGTGGCAGCCAGCTGTGGCAGAGAAAACACACAAGGAAAGAGC	3600
Db	3541		
Qy	3601	ACCCAGGACTGTCTATATGGAAGAAAACAGGACTGCAACTCACCTTCACAAAATGAGGA	3660
Db	3601		
Qy	3661	CCAGACACGCTCATGTATGAGTTGATGACGGTGTGGAGCCCTCAACATCCTGCTCCC	3720
Db	3661		
Qy	3721	CTCTACTACACATGGTTAAGCCCTTTGCTCTGCTCCAGGTTTCACACTCTCTGCACTA	3780
Db	3721		
Qy	3781	CCTCTTCATGGGTGCCTCAGACAGACACTTGCTCTTCCCTTTGAAAGCTTTGGGCTA	3840
Db	3781		
Qy	3841	CGTGGATGACCAGCTGTTCTGTTCTATGATNATGAGAGTCCCGCTGTGGAGCCCGGAAC	3900
Db	3841		
Qy	3901	TCCATGGGTTTCCAGTAGAAATTTTCAGCCAGATGTGGCTGCAGCTGAGTCTAGACTCTGAA	3960
Db	3901		
Qy	3961	AGGTTGGGATCACATGTTCACTCTTGACTTCTGGACTATTATGGAATAATCACACACACAG	4020
Db	3961		
Qy	4021	CAAGGGTATGTGGAGAGGGGGCCCTACCTTCCTCAGGTTGTCTCAGAGCTTTTCATCTTTTC	4080
Db	4021		
Qy	4081	ATGCATCTTGAAGAAACACCTGGAGCTGTGAGTCTTGTGGGACACGGGAAGGGAAG	4140
Db	4081		
Qy	4141	GAATTTGCTCCTCAGATCATTTTGGTCCCTTGGGGATGTGGAAATAGGGAATATTCCTT	4200

	D	b	4141	GAAATTTGCTTCCGTAGATCATTTGGTCCTTGCGGATGGTGGAAATAGGACACTATTCTCTT	4200
	Q	y	4201	TGGTTGCAGTTTAACAAGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAAGTCATCCTTG	4260
	D	b	4201	TGGTTGCAGTTTAACAAGCTGGGGATTTTTCCAGAGTCCCACACCCTGCAAGTCATCCTTG	4260
	Q	y	4261	GGCTGTGAATGCAAGAACAACAAGTAGTACCAGAGGCCCTACTTGGAAGTACGGGTATGATGG	4320
	D	b	4261	GGCTGTGAATGCAAGAACAACAAGTAGTACCAGAGGCCCTACTTGGAAGTACGGGTATGATGG	4320
	Q	y	4321	CAGGACCACTTCGAA'TCT'GCCCTGACACACTTGGATTGGAGACAGCACAGAACCCAGGGCC	4380
	D	b	4321	CAGGACCACTTCGAA'TCT'GCCCTGACACACTTGGATTGGAGACAGCACAGAACCCAGGGCC	4380
	Q	y	4381	TGGCCCCAAGCTGGAGTGGGAAAAGGCACAAGATTCCGGGCCAGGCAGAACACAGGGCCTAC	4440
	D	b	4381	TGGCCCCAAGCTGGAGTGGGAAAAGGCACAAGATTCCGGGCCAGGCAGAACACAGGGCCTAC	4440
	Q	y	4441	CTGGAGAGGAC'TGCCCTGCACAGCTGCAGCAGTTGCTTGGAGCTTGGGACAGAGTGTTTIG	4500
	D	b	4441	CTGGAGAGGAC'TGCCCTGCACAGCTGCAGCAGTTGCTTGGAGCTTGGGACAGAGTGTTTIG	4500
	Q	y	4501	GACCAACAAGTATGTTGGAAAAACACACTTCTGCCOCTATACTCTAGTGGCAGAGTGGAGG	4560
	D	b	4501	GACCAACAAGTATGTTGGAAAAACACACTTCTGCCOCTATACTCTAGTGGCAGAGTGGAGG	4560
	Q	y	4561	AGTTTGCAGGCGACGAATCCCTGGTGGAGTTTCAGAGSTGGCTGAGGCTGTGTGCCTC	4620
	D	b	4561	AGTTTGCAGGCGACGAATCCCTGGTGGAGTTTCAGAGSTGGCTGAGGCTGTGTGCCTC	4620
	Q	y	4621	TCCAATATCTGGGAAGGACTTCTCAATPCTTAGASTCTCTACCTTATAATTTAGATGTA	4680
	D	b	4621	TCCAATATCTGGGAAGGACTTCTCAATPCTTAGASTCTCTACCTTATAATTTAGATGTA	4680
	Q	y	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTCTCCATGCATATGGCTCAAAGGAA	4740
	D	b	4681	TGAGACAGCCACAAGTCATGGGTTTAATTTCTTCTCCATGCATATGGCTCAAAGGAA	4740
	Q	y	4741	GTGTCTATGGCCCTTGCTTTTTATTAAACCAATAATCTTTTGTATATTATACCTGTAA	4800
	D	b	4741	GTGTCTATGGCCCTTGCTTTTTATTAAACCAATAATCTTTTGTATATTATACCTGTAA	4800
	Q	y	4801	AAATTCAGAAATGTCAAGCGCGGCACGGTGGCTCACCCCTGTATCCACGACCTTTGGG	4860
	D	b	4801	AAATTCAGAAATGTCAAGCGCGGCACGGTGGCTCACCCCTGTATCCACGACCTTTGGG	4860
	Q	y	4861	AGGCGAGCGGGTGFTCAAGGTCAGAGTTTGAGACACGCCCTGACCAACATGTTGCAA	4920
	D	b	4861	AGGCGAGCGGGTGFTCAAGGTCAGAGTTTGAGACACGCCCTGACCAACATGTTGCAA	4920
	Q	y	4921	ACCCGTCTCTAAAAAATAACAAAAATTAGCTGGTCCACAGTCATGGCGACCTGTAGTCCCA	4980
	D	b	4921	ACCCGTCTCTAAAAAATAACAAAAATTAGCTGGTCCACAGTCATGGCGACCTGTAGTCCCA	4980
	Q	y	4981	GCTAATTTGGAGGCTGAGGCAGAGCATCGCTTGAACCTTGGGAAGCGAAGTTCACACTGA	5040
	D	b	4981	GCTAATTTGGAGGCTGAGGCAGAGCATCGCTTGAACCTTGGGAAGCGAAGTTCACACTGA	5040
	Q	y	5041	GCCAAGATCGGCCACTTGCACTCCAGCCTAGGCAGAGAGTGCAGACTCCATCTTTAAAAA	5100
	D	b	5041	GCCAAGATCGGCCACTTGCACTCCAGCCTAGGCAGAGAGTGCAGACTCCATCTTTAAAAA	5100
	Q	y	5101	AAAAAAAAAAAAAAAAAGAGAAATTCAGAGATCTCAGAGTATCATATGATTAACAGACAAA	5160
	D	b	5101	AAAAAAAAAAAAAAAAAGAGAAATTCAGAGATCTCAGAGTATCATATGATTAACAGACAAA	5160
	Q	y	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGSTTTAAAAGTTCTTTTCAT	5220
	D	b	5161	ATATCAAGTGAGGCCACTTATCAGAGTAGAAGATCCTTTAGSTTTAAAAGTTCTTTTCAT	5220
	Q	y	5221	AGAACATAGCAATATCACTGAAGCTACCTTATCTTACAAGTCGCTTCTTATAACAATGTC	5280

Db	5221	AGACATAGCAATTAATCACTGAAGCTACCTATTCTTACAAAGTCCGCTCTCTTATAACAATGC	528
Qy	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCACTGTATTTCAATCAATTTTCAATGACACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCACTGTATTTCAATCAATTTTCAATGACACATAA	5340
Qy	5341	AGGCAATTTTATCTATTCAGAACAAAGACATGGGTAAACAGATATGTATAATTTACATGTG	5400
Db	5341	AGGCAATTTTATCTATTCAGAACAAAGACATGGGTAAACAGATATGTATAATTTACATGTG	5400
Qy	5401	AGGAGAACAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTAGAGTCCAATTTTGG	5460
Db	5401	AGGAGAACAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTAGAGTCCAATTTTGG	5460
Qy	5461	ACACAAAATGGTGCTCTCCTGTAGCTTGTCTTTTCTGAAAAGGGTATTTCCCTTCCTCC	5520
Db	5461	ACACAAAATGGTGCTCTCCTGTAGCTTGTCTTTTCTGAAAAGGGTATTTCCCTTCCTCC	5520
Qy	5521	AACCTATAGAGGAAGTGAAAGTTCCAGTCTTCTCTGGCAAGGGTAAACAGATCCCTCTC	5580
Db	5521	AACCTATAGAGGAAGTGAAAGTTCCAGTCTTCTCTGGCAAGGGTAAACAGATCCCTCTC	5580
Qy	5581	CTCATCTCTCTCTTCTCTCAAGTGCCCTCTTCTTGGTGAAGGTGACATCATGTGACC	5640
Db	5581	CTCATCTCTCTCTTCTCTCAAGTGCCCTCTTCTTGGTGAAGGTGACATCATGTGACC	5640
Qy	5641	TCCTTCAGTGACCACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATG	5700
Db	5641	TCCTTCAGTGACCACTCTACGGTGTGGGGCTTTGAATCTACTACCCCGAGAACATCACCATG	5700
Qy	5701	AAGTGGCTGAAGGATAAGCAGCCATGGATGCCAAGGAGTTTCGAACCTTAAGACGTATTG	5760
Db	5701	AAGTGGCTGAAGGATAAGCAGCCATGGATGCCAAGGAGTTTCGAACCTTAAGACGTATTG	5760
Qy	5761	CCCAATGGGATGGGACCTTACCAGGCTCGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Db	5761	CCCAATGGGATGGGACCTTACCAGGCTCGATTAACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATACGTNCCAGGTGAGCACCCAGGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATACGTGCCAGGTGGAGCACCCAGGCCCTGGATCAGCCCTCATTTGTGATCTGG	5880
Qy	5881	GGTATGTGATGTATGAGAGCCAGGAGCTGAGAAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
Db	5881	GGTATGTGATGTATGAGAGCCAGGAGCTGAGAAAAATCTATTGGGGGTTGAGAGGAGTGCC	5940
Qy	5941	TGAGGAGGTAAATTTATGGCAGTGAGATGAGGATCTCCTCTTTTGTAGGGGGTGGGCTGAGG	6000
Db	5941	TGAGGAGGTAAATTTATGGCAGTGAGATGAGGATCTCCTCTTTTGTAGGGGGTGGGCTGAGG	6000
Qy	6001	GTGCAATCAAAGGCTTTAACTTGCTTTTTCGTGTTTATAGACCCTCACCCTCTGGCACCC	6060
Db	6001	GTGCAATCAAAGGCTTTAACTTGCTTTTTCGTGTTTATAGACCCTCACCCTCTGGCACCC	6060
Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTCTCATCTTGTTCATTGGAAATTT	6120
Db	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTCTCATCTTGTTCATTGGAAATTT	6120
Qy	6121	TGTTTCATTAATTTAAGGAAGAGCGAGGTTTCAAGTGAAGTAGGAACAAGGGGGAGTCTCT	6180
Db	6121	TGTTTCATTAATTTAAGGAAGAGCGAGGTTTCAAGTGAAGTAGGAACAAGGGGGAGTCTCT	6180
Qy	6181	TAGTACCTCTGCCCGACAGGTGGAAGAGGGGACAGGGGATCTGGCATCCCATGG	6240
Db	6181	TAGTACCTCTGCCCGACAGGTGGAAGAGGGGACAGGGGATCTGGCATCCCATGG	6240
Qy	6241	AAGCATTTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
Db	6241	AAGCATTTTTCTCATTTATATTCTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAAT	6300
Qy	6301	AATGGTTCTCCCGAAGTGAAGTCTTAATTCACAAACATCTTCAAGACACCTACTAT	6360
Db	6301	AATGGTTCTCCCGAAGTGAAGTCTTAATTCACAAACATCTTCAAGACACCTACTAT	6360

QY	6361	TTTCAAGACAGCTGTTTAAGGTAGTACAGGGGCTTTTGAGGTTGAGAAGTCACTGTGGCTAT	6420
DB	6361	TTTGCAGAGCTGTTTAAGGTAGTACAGGGGCTTTTGAGGTTGAGAAGTCACTGTGGCTAT	6420
QY	6421	TCTCAGAACCAATCTGGTAGGGAATGAAATGATAGCAAGTAATGTAGTTAAAGAG	6480
DB	6421	TCTCAGAACCAATCTGGTAGGGAATGAAATGATAGCAAGTAATGTAGTTAAAGAG	6480
QY	6481	ACCCCATGAGTCTTAAAGCAGCAGCAAGCAAAATGCTTTAGGGTCTCAAGGAAAGAAATG	6540
DB	6481	ACCCCATGAGTCTTAAAGCAGCAGCAAGCAAAATGCTTTAGGGTCTCAAGGAAAGAAATG	6540
QY	6541	ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA	6600
DB	6541	ATCACATTCAGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA	6600
QY	6601	TTAGGTGAGGTTGAAGATGATGGAGGTCTACACAGACGAGCAACCATGCCAAGTAGGA	6660
DB	6601	TTAGGTGAGGTTGAAGATGATGGAGGTCTACACAGACGAGCAACCATGCCAAGTAGGA	6660
QY	6661	GAGTATAGGCGATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTGCGT	6720
DB	6661	GAGTATAGGCGATACTGGGAGATTAGAAATAATTACTGTACCTTAACCCCTGAGTTGCGT	6720
QY	6721	AGCTATCACTCACCAATTATGCATTTCTACCCCTGACATCTGTGGTAGGGAAGA	6780
DB	6721	AGCTATCACTCACCAATTATGCATTTCTACCCCTGACATCTGTGGTAGGGAAGA	6780
QY	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGCTCTTTTGGGATATTGGGTTATGA	6840
DB	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGCTCTTTTGGGATATTGGGTTATGA	6840
QY	6841	TCAGTGGGTCATTAAGGATCCCTAAGAAAGGAGGACCGATCTCCCTTATATGGTG	6900
DB	6841	TCAGTGGGTCATTAAGGATCCCTAAGAAAGGAGGACCGATCTCCCTTATATGGTG	6900
QY	6901	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCCAGTTAGAAAGCCCAATAAGCAT	6960
DB	6901	AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGACCCAGTTAGAAAGCCCAATAAGCAT	6960
QY	6961	TTCCAGATGAGAGTAATGTTCTTCAAAATCCAATAGTGGCCAGGTCTAAATTCAGATGG	7020
DB	6961	TTCCAGATGAGAGTAATGTTCTTCAAAATCCAATAGTGGCCAGGTCTAAATTCAGATGG	7020
QY	7021	GTGAATCAGGAAATAAGGAAGAGAAAGCAAGATGGTGCCTTAGGTCTTGTGATGCCT	7080
DB	7021	GTGAATCAGGAAATAAGGAAGAGAAAGCAAGATGGTGCCTTAGGTCTTGTGATGCCT	7080
QY	7081	CTTTCTCTGGTCTTGTCTCCACAGGAGGACCCATGGGCACTACGCTTTAGCTGAACG	7140
DB	7081	CTTTCTCTGGTCTTGTCTCCACAGGAGGACCCATGGGCACTACGCTTTAGCTGAACG	7140
QY	7141	TGAGTGACGCGACCTGCAGACTACTGTGGGAGGAGACAAACATAGAGACTCAAGA	7200
DB	7141	TGAGTGACGCGACCTGCAGACTACTGTGGGAGGAGACAAACATAGAGACTCAAGA	7200
QY	7201	GGGAGTGCATTTATGAGCTCTTCAATGTTTCAGGAGAGAGTTGAACTTAAACATAGAAATT	7260
DB	7201	GGGAGTGCATTTATGAGCTCTTCAATGTTTCAGGAGAGAGTTGAACTTAAACATAGAAATT	7260
QY	7261	GCCTGAGCAACTCTTGAATTTAGCCTCTCTGTTCAATTCCTCAGAAAGATTTCCCAT	7320
DB	7261	GCCTGAGCAACTCTTGAATTTAGCCTCTCTGTTCAATTCCTCAGAAAGATTTCCCAT	7320
QY	7321	TTAGGTTTCTGAGTTCCATGATGCCGGTGATCCCTTAGCTGTGACCTCTCCCTGGAACCTG	7380
DB	7321	TTAGGTTTCTGAGTTCCATGATGCCGGTGATCCCTTAGCTGTGACCTCTCCCTGGAACCTG	7380
QY	7381	TCCTCATGAACTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCGTCACCTCAGAG	7440
DB	7381	TCCTCATGAACTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCGTCACCTCAGAG	7440

[illegible]

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QY 9661 TGAATAACTATTAAACACTTGCTATTACCTGTTAGTATTATTGTTGCAATTAATAATGCA 9720
Db 9661 TGAATAACTATTAAACACTTGCTATTACCTGTTAGTATTATTGTTGCAATTAATAATGCA 9720
QY 9721 TATACATTTAATAATATGATATTGTTATGATCTGATGATGATTTATGAAGTTCCTGTTTC 9780
Db 9721 TATACATTTAATAATATGATATTGTTATGATCTGATGATGATTTATGAAGTTCCTGTTTC 9780
QY 9781 ATCTTGATATATACATTAATCGCTTGCTCATTTTGGAGACATTTATTTTGCTTCAATTT 9840
Db 9781 ATCTTGATATATACATTAATCGCTTGCTCATTTTGGAGACATTTATTTTGCTTCAATTT 9840
QY 9841 CTTTACATTTTGCTTTACGGAATATTTTCATTCAACTGTGTAGCGGAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGCTTTACGGAATATTTTCATTCAACTGTGTAGCGGAATTAATCGTGT 9900
QY 9901 TCTTCACTCTAGGACATTTGCTCTAAGTTTGAAGACATTTGTTTATTACCAGCAAC 9960
Db 9901 TCTTCACTCTAGGACATTTGCTCTAAGTTTGAAGACATTTGTTTATTACCAGCAAC 9960
QY 9961 CATCTGAAAGCATATGACAAATATTTCTCTCTTAATCTTACTATCTACTGAAAGCAGA 10020
Db 9961 CATCTGAAAGCATATGACAAATATTTCTCTCTTAATCTTACTATCTACTGAAAGCAGA 10020
QY 10021 CTGCTATAAGGCTTCACITACCTCTCTACCTCATAGGAATAGTTACAATTAATTTAT 10080
Db 10021 CTGCTATAAGGCTTCACITACCTCTCTACCTCATAGGAATAGTTACAATTAATTTAT 10080
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Db 10141 CCAGTCTTCACAGTAACACATTTTCACTAACACATTTACTAACATCAGCAACTGTGGCT 10200
QY 10201 GTTAATTTTTTAAAGAAATTTAAGTCCCTCATTTTCTTCGGTGTGTTTTTAAGCTTAA 10260
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RESULT 6
LOCUS ARL149460 10825 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6228594.
ACCESSION ARL149460
VERSION ARL149460.1 GI:15114051
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknwn.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
JOURNAL Patent: US 6228594-A 3 08-MAY-2001;
FEATURES Location/Qualifiers
source 1. .10825
BASE COUNT 2999 a 2253 c 2647 g 2926 t
ORIGIN

Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TCTAAGCTTCAGATATAAATTTTAAATGTATGATTGAATTTTGAATTTTGAATATATAATTTA 60
QY 61 AATATCTAAAGTTTCAGATCAGACATTCGAAAGCTACTTTCCCAATCAACAACACCCCT 120
Db 61 AATATCTAAAGTTTCAGATCAGACATTCGAAAGCTACTTTCCCAATCAACAACACCCCT 120
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGATCACCTAGTGTGTTTCACAGCAGGTACCTT 180
Db 121 TCAGGATTTAAAAACCAAGGGGACACTGATCACCTAGTGTGTTTCACAGCAGGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACAGGAAGTT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTGCTTTTCCACAGGAAGTT 240
QY 241 TTACTGGCATCTCTCAGCCTAGGCAATAGCTGTAGGTTGACTTCTGGAGCCATCCCG 300
Db 241 TTACTGGCATCTCTCAGCCTAGGCAATAGCTGTAGGTTGACTTCTGGAGCCATCCCG 300
QY 301 TTTCCCGCCCCCAAAAGAGCGAGATTTAACGGGACGTGCGGCCAGAGCTGGGGAA 360
Db 301 TTTCCCGCCCCCAAAAGAGCGAGATTTAACGGGACGTGCGGCCAGAGCTGGGGAA 360
QY 361 ATGGGCGCGGAGCCAGCGCGGCTTCCTCTCTGATGCTTTTGCAGACCGCGGTCCTG 420
Db 361 ATGGGCGCGGAGCCAGCGCGGCTTCCTCTCTGATGCTTTTGCAGACCGCGGTCCTG 420
QY 421 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTCGGGCGCAACTAGGGCGCGCGGGGTG 480
Db 421 CAGGGCGCTTGCTGCTGAGTCCGAGGGCTCGGGCGCAACTAGGGCGCGCGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTTTTCCTTGGGAGTTTGTAACTTTGGAGGACCTGC 540
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QY 541 TCAACCCATCCGAAGCCCTCTCCCTACTTTCTCGCTCCAGACCCCGTAGGAGTGC 600
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 QY 601 CTACCACTGAACCTGCAGATAGGGGTCCCTCGCCCGAGGACCTGCCCCCTCCCGGCGCTG 660
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 Db 781 AACTCGGGTTTATTTCCAAATGTCAGCTGTGCAGTCTTTTCCCCAGTCATCTCCAAACAGG 840
 QY 841 AAGTTCCTCCCTGAGTGCTTTGCCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG 900
 Db 841 AAGTTCCTCCCTGAGTGCTTTGCCGAGAAGGCTGAGCAAAACCCACAGCAGGATCCGCACGG 900
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 QY 1321 GGAATTCAGATTATTAACCTTTTTCAGGTTTACAAAGACATAAATAATCTGTTTTCTG 1380
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 QY 1381 ATGTTATTTCAAGTACTACAGCTCTTCTAATCTTAGTTGACAGTGAATTTGGCCCTGTAG 1440
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 Db 1441 TGTAGCAGAGTTCCTGTTGGGTACACCGGCTCAGCAGCAGCTTTTGAGTTTTCGTA 1500
 QY 1501 CTAGCTGTATCCACATTTTACACATGACAAGAATGAGGATGGCAGCGCTGCTTCCTGG 1560
 Db 1501 CTAGCTGTATCCACATTTTACACATGACAAGAATGAGGATGGCAGCGCTGCTTCCTGG 1560
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Db 1621 TATGATTCTTAAACATCACACTGATTTAGAGTTGAATAATAAAATTTCAITGTTGACAG 1680
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 QY 1741 CAAGGAGAGAGCAGGAGAAACAAGTCTTTTACCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
 Db 1741 CAAGGAGAGAGCAGGAGAAACAAGTCTTTTACCTTTGATATTTTGCATTTCTAGTGGGAGA 1800
 QY 1801 GATGACAATAAGCAAAATGAGCAGAGAAAGATATACAACTACAGAAATCATGGCTGTTGTA 1860
 Db 1801 GATGACAATAAGCAAAATGAGCAGAGAAAGATATACAACTACAGAAATCATGGCTGTTGTA 1860
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 Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGGTGCACCTTGAGCAGAGACATGAAGGA 1920
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 Db 2281 GCCACAAACAAAGTGTGCAGGCGCTGTAGGCTGTGGTGAATTTCTAGCCAAGGAGTA 2340
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 Db 2401 AAGGGAGCAACAGTAAAGCAGGAGCCCGCAGCAGGAGCTTTACACAGTCCAGGCAAG 2460
 QY 2461 AGGTAGTCAGTGGCTGGGTGGGAACAAAGGAGTGACAAAACCAATTTGCTCCTGAA 2520
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 Db 2581 CTGGGTGTAGTAGCTCATGCCAAGGAGGAGCCCAAGGAGCAGATTTCTGAGCTCAGGA 2640
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 Db 2641 GTTCAAGACAGCCTGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
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Db	2701	GCTGGGTGTTGGTGGCATGCACCTGTGTATCTTAGCTACTTCGGAGGAGCCGTGAGGTGGAGGGTA	2760
Qy	2761	TTGCTTGAGCCCCAGGAAGTTGAGGCTGCGAGTCAGCATTAGCTGTGCCACTGTACTTTCAGC	2820
Db	2761	TTGCTTGAGCCCCAGGAAGTTGAGGCTGCGAGTCAGCATTAGCTGTGCCACTGTACTTTCAGC	2820
Qy	2821	CTAGGTGCAGAGCAGACCCTGCTCCCTCTGACCCCCTGAAAGAGACAGATGTTAAAGT	2880
Db	2821	CTAGGTGCAGAGCAAGACCCTGTCTCCCTTGACCCCCTGAAAGAGAGAGATTTAAAGT	2880
Qy	2881	TGACTTTGTCTTTATTTAATTTTATTATTTGGCCTGAGCAGTGGGTAATTTGSCAATGCCAT	2940
Db	2881	TGACTTTGTCTTTATTTAATTTTATTATTTGGCCTGAGCAGTGGGTAATTTGSCAATGCCAT	2940
Qy	2941	TTCTGAGATGGTGAAGCAGAGGAAGAGCAGTTTGGGTAAATTC AAGGATCTGCATTTCG	3000
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Qy	3001	GGACATGTTAAGTTTGAGATTC CAGCTCAGGCTTCCAAGTGTGAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAGTTTGAGATTC CAGCTCAGGCTTCCAAGTGTGAGGCCACATAGGCAGTT	3060
Qy	3061	CAGTGTAAAGAATTCAGCACCAAAGGCTGGSCAGGTGGCTCACTTCTGTAAATCC CAGCACT	3120
Db	3061	CAGTGTAAAGAATTCAGCACCAAAGGCTGGSCAGGTGGCTCACTTCTGTAAATCC CAGCACT	3120
Qy	3121	TTGGTGGCTCAGGCAGGTGATCATT TGAGTFCAGGAGTTTGAGACAAGCTTTGGCCAAACA	3180
Db	3121	TTGGTGGCTCAGGCAGGTGATCATT TGAGTFCAGGAGTTTGAGACAAGCTTTGGCCAAACA	3180
Qy	3181	TGGTGA AACCCCATGTCTACTAAAAATACAAAATTTAGCCTGGTGTGTTGGCGCACGCCCT	3240
Db	3181	TGGTGA AACCCCATGTCTACTAAAAATACAAAATTTAGCCTGGTGTGTTGGCGCACGCCCT	3240
Qy	3241	ATAGTCCCAGGTTTTTCAGGAGGTTTAGT TAGGAGAAATCCCTTGAACCCAGGAGGTGCAGG	3300
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Db	3301	TTGCAGTGCAGCTGAGATTTGTCAC TGCAC TCCAGCCTGGGTGATAGAGTGCAGACTCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTTCTCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTTCTCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGGCCCTGAGCACCAACTCCTGAGTTTCAACTACCATGGCTAGACACACTTTAAC	3480
Db	3421	TCTAATTTGGCCCTGAGCACCAACTCCTGAGTTTCAACTACCATGGCTAGACACACTTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTTGGAATAGGAT	3540
Db	3481	ATTTTCTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTTGGAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAAGGGGTGGCAGCCACTGTGGCAGAGAAAAGCACACAAGGAAGAGC	3600
Db	3541	CTGGGGCAGTGAAGGGGTGGCAGCCACTGTGGCAGAGAAAAGCACACAAGGAAGAGC	3600
Qy	3601	ACCCAGGACTGT CATATGGAAGAAAAGACAGGACTGCAACTCACCCCTTCACAAAATGAGGA	3660
Db	3601	ACCCAGGACTGT CATATGGAAGAAAAGACAGGACTGCAACTCACCCCTTCACAAAATGAGGA	3660
Qy	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGGAGCCCTCAACATCTCTGCTCCC	3720
Db	3661	CCAGACACAGCTGATGGTATGAGTTGATGCAGGTGTGGAGCCCTCAACATCTCTGCTCCC	3720
Qy	3721	CTCCTACTACACATGGTTAAGGCCTCTGTCTGTCTCCAGGTTTCACACTCTCTGCACATA	3780
Db	3721	CTCCTACTACACATGGTTAAGGCCTCTGTCTGTCTCCAGGTTTCACACTCTCTGCACATA	3780
Qy	3781	CCTCTTCATGGGTGCCTCAGACAGGACCTCTGGTCTTTTCTTCTTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCATGGGTGCCTCAGACAGGACCTCTGGTCTTTTCTTCTTTTGAAGCTTTGGGCTA	3840

3841	QY	CGTGGATGACCAAGCTGTTCTGTCTTATGATNATGAGAGTCGCCGTGGAGACCCCGAAC	3900
3841	DB	CGTGGATGACCAAGCTGTTCTGTCTTATGATCATGAGAGTCGCCGTGGAGACCCCGAAC	3900
3901	QY	TCCATGGGTTCCCACTAGAAATTCAAAGCCAGAGTGGGCTGCAGCTGAGTCAAGACTCTGAA	3960
3901	DB	TCCATGGGTTCCCACTAGAAATTCAAAGCCAGAGTGGGCTGCAGCTGAGTCAAGACTCTGAA	3960
3961	QY	AGGCTGGGATACATGTTCTACTGTTGACATCTGGAATATATGGAANATCAACACCACAG	4020
3961	DB	AGGCTGGGATACATGTTCTACTGTTGACATCTGGAATATATGGAANATCAACACCACAG	4020
4021	QY	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGGTGTGCAGAGCTTTTCATCTTTTC	4080
4021	DB	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGGTGTGCAGAGCTTTTCATCTTTTC	4080
4081	QY	ATGCATCTTGAGGAACACGCTGGAGTCTGAGGTCCTGTCGGAGCAGGGAAGAGGAAG	4140
4081	DB	ATGCATCTTGAGGAACACGCTGGAGTCTGAGGTCCTGTCGGAGCAGGGAAGAGGAAG	4140
4141	QY	GAATTTGCTTCCTGAGATCAATTTGGTCCCTGGGGATGTGGAATATAGGACCTATTCTT	4200
4141	DB	GAATTTGCTTCCTGAGATCAATTTGGTCCCTGGGGATGTGGAATATAGGACCTATTCTT	4200
4201	QY	TGCTGCAGTTACAGAGCTGGGGAATTTTCCAGAGTCCCAACCCCTCAGGTCATCTCG	4260
4201	DB	TGCTGCAGTTACAGAGCTGGGGAATTTTCCAGAGTCCCAACCCCTCAGGTCATCTCG	4260
4261	QY	GGCTGTGAATGCAAGGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
4261	DB	GGCTGTGAATGCAAGGAACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
4321	QY	CAGGACCACTTGAATTCCTGCCCTGACACACTGGATTTGGAGAGCAGACAGCCAGGGCC	4380
4321	DB	CAGGACCACTTGAATTCCTGCCCTGACACACTGGATTTGGAGAGCAGACAGCCAGGGCC	4380
4381	QY	TGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTCGGGCCAGGCAGACAGGGCCCTAC	4440
4381	DB	TGGCCCAACCAAGCTGGAGTGGGAAGGCAACAAGATTCGGGCCAGGCAGACAGGGCCCTAC	4440
4441	QY	CTGGAGAGGGACTGCCCTGCACAGCTGCAGAGTTCTGAGCTGGGAGAGGTGTTTGG	4500
4441	DB	CTGGAGAGGGACTGCCCTGCACAGCTGCAGAGTTCTGAGCTGGGAGAGGTGTTTGG	4500
4501	QY	GACCAACAAGGTATGTGGAAACACACTTCTGCCCCATACCTCTAGTGGCAGAGTGGAGG	4560
4501	DB	GACCAACAAGGTATGTGGAAACACACTTCTGCCCCATACCTCTAGTGGCAGAGTGGAGG	4560
4561	QY	AGGTTGACAGGCAACCGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCC	4620
4561	DB	AGGTTGACAGGCAACCGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCC	4620
4621	QY	TCCAAATTTCTGGGAAGGCACTTCTCAATCCTAGAGTCTCTACCTTTAATTTGAGATGTA	4680
4621	DB	TCCAAATTTCTGGGAAGGCACTTCTCAATCCTAGAGTCTCTACCTTTAATTTGAGATGTA	4680
4681	QY	TGAGACGCCACAAGTCAATGGGTTTAATTTCTTTCTCCATCATGCTATGGCTCAAAAGGAA	4740
4681	DB	TGAGACGCCACAAGTCAATGGGTTTAATTTCTTTCTCCATCATGCTATGGCTCAAAAGGAA	4740
4741	QY	GTGTCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGATTTATATACCTGTTAA	4800
4741	DB	GTGTCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGATTTATATACCTGTTAA	4800
4801	QY	AAATTCAGAAATGTCAAGCGCGGACGGTGCATCCCTCTTAATCCACGACCTTTGGG	4860
4801	DB	AAATTCAGAAATGTCAAGCGCGGACGGTGCATCCCTCTTAATCCACGACCTTTGGG	4860
4861	QY	AGGCCGAGCGGGGTGGTCAACAAGTTCAGAGTGTGAGACGACCGCTGACCAACATGGTGAA	4920
4861	DB	AGGCCGAGCGGGGTGGTCAACAAGTTCAGAGTGTGAGACGACCGCTGACCAACATGGTGAA	4920

Qy	4921	ACCCGTCCTCTAAAAAAATACAAAAATTTAGCTGGTGCACAGTCAATGCGCACCTCTAGTCCCA	4980
Db	4921	ACCCGTCCTCTAAAAAAATACAAAAATTTAGCTGGTGCACAGTCAATGCGCACCTCTAGTCCCA	4980
Qy	4981	GCTAATTGAAGGCTGAGCGCAGGAGCATCGCTTCAACCTGGGAAGCGGAAGTTGCACATGA	5040
Db	4981	GCTAATTGAAGGCTGAGCGCAGGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACATGA	5040
Qy	5041	GCCCAAGATCGCCCACTGCACCTCCAGCTAGGCAGCAGAGTGAGATCCCATCTTAAAAA	5100
Db	5041	GCCCAAGATCGCCCACTGCACCTCCAGCTAGGCAGCAGAGTGAGATCCCATCTTAAAAA	5100
Qy	5101	AAAAAATAAGAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCAAGACAAA	5160
Db	5101	AAAAAATAAGAGAGAAATTCAGAGATCTCAGCTATCATATGAATACCAAGACAAA	5160
Qy	5161	ATATCAAGTGAGGCCATTATCAGAGTAGAAGATCCCTTTAGGTTAAAAAGTTTCTTTTCAT	5220
Db	5161	ATATCAAGTGAGGCCATTATCAGAGTAGAAGATCCCTTTAGGTTAAAAAGTTTCTTTTCAT	5220
Qy	5221	AGAACATAGCAATATACACTGAAGCTACCTATCTTCAAGTCGCTTCTTTATACAAATGC	5280
Db	5221	AGAACATAGCAATATACACTGAAGCTACCTATCTTCAAGTCGCTTCTTTATACAAATGC	5280
Qy	5281	CTCCTAGGTTGACCCAGGTGAACCTGACCATCTGTTTCAATCATTTTCAATGCACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAACCTGACCATCTGTTTCAATCATTTTCAATGCACATAA	5340
Qy	5341	AGGCAATTTTATCTATCAGAACAAAGAACATGGGTACAGATATGATATTTACATGTG	5400
Db	5341	AGGCAATTTTATCTATCAGAACAAAGAACATGGGTACAGATATGATATTTACATGTG	5400
Qy	5401	AGGAGACAGCTGATCTGACCTGCTCCAAAGTGACACTGTTGTAGAGTCCCAATCTTAGG	5460
Db	5401	AGGAGACAGCTGATCTGACCTGCTCCAAAGTGACACTGTTGTAGAGTCCCAATCTTAGG	5460
Qy	5461	ACACAAATGGTGCTCTCCTCTAGCTTGTTTTTCTGAAAAAGGTATTTCTCTCTCTCC	5520
Db	5461	ACACAAATGGTGCTCTCCTCTAGCTTGTTTTTCTGAAAAAGGTATTTCTCTCTCTCC	5520
Qy	5521	AACCTATAGAACGATGAAGATTCACGTCCTCTGCGCAAGGGTAAACAGATCCCCTCTC	5580
Db	5521	AACCTATAGAACGATGAAGATTCACGTCCTCTGCGCAAGGGTAAACAGATCCCCTCTC	5580
Qy	5581	CTCATCTCTCTCTTCTCCTGTCAAGTGCTCTTTGTGGAAGGTGACACATCATGTGACC	5640
Db	5581	CTCATCTCTCTCTTCTCCTGTCAAGTGCTCTTTGTGGAAGGTGACACATCATGTGACC	5640
Qy	5641	TCCTCAGTGACCACTACAGGCTCGGGGCTTGAACCTACTACCCCCAGAACATCACCATG	5700
Db	5641	TCCTCAGTGACCACTACAGGCTCGGGGCTTGAACCTACTACCCCCAGAACATCACCATG	5700
Qy	5701	AAAGTGGCTGAAGGATAGCAGCCAAATGGATGCCAAGGAGTTTCGAACCTAAAGACGTATTG	5760
Db	5701	AAAGTGGCTGAAGGATAGCAGCCAAATGGATGCCAAGGAGTTTCGAACCTAAAGACGTATTG	5760
Qy	5761	CCCAATGGGGATGGACCTTACAGGCTCGGATACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Db	5761	CCCAATGGGGATGGACCTTACAGGCTCGGATACCTTTGGCTGTACCCCTGGGGAAGAG	5820
Qy	5821	CAGAGATATAGTNCAGGTGGAGCACCCAGAGCTGGATCAGCCCTCATTTGTGATCTGG	5880
Db	5821	CAGAGATATAGTNCAGGTGGAGCACCCAGAGCTGGATCAGCCCTCATTTGTGATCTGG	5880
Qy	5881	GGATGTGACTGATGAGAGCCAGGACTGAGAAAATCTATTGGGGGTTGAGAGAGTGC	5940
Db	5881	GGATGTGACTGATGAGAGCCAGGACTGAGAAAATCTATTGGGGGTTGAGAGAGTGC	5940
Qy	5941	TCAGAGGTAATATTGCGAGTGAGATGAGGATCTGCTTTCTTAGGGGGTGGGCTGAGG	6000
Db	5941	TCAGAGGTAATATTGCGAGTGAGATGAGGATCTGCTTTCTTAGGGGGTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAGGCTTTAACTTGTCTTTTAGAGCCCTACCGCTTGCACCC	6060

Db	6001	GTGGCAATCAAAGGCTTTAACTTGCTTTTCTGTTTAGAGCCCTCACCGTCTGGCACCC	6060
Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCFATCTTTGTTTCATTGGAAATTT	6120
Db	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCFATCTTTGTTTCATTGGAAATTT	6120
Qy	6121	TGTTCAATAATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGTAGGAACAAAGSGGAAGTCTCT	6180
Db	6121	TGTTCAATAATTAAGGAAGAGGCAGGGTTCAAGTGAGTAGTAGGAACAAAGSGGAAGTCTCT	6180
Qy	6181	TAGTACTCTGCCACAGGSCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACTCTGCCACAGGSCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG	6240
Qy	6241	AAGCATTTTCTCAATTAATATTTCTTTGGGGACACAGACGCTCCCTGGGAGACAGAAAT	6300
Db	6241	AAGCATTTTCTCAATTAATATTTCTTTGGGGACACAGACGCTCCCTGGGAGACAGAAAT	6300
Qy	6301	AATGGTTCCTCCCAAGATGAAGTCTCTAAATCAACAACATCTTCAGAGCACCTACTAT	6360
Db	6301	AATGGTTCCTCCCAAGATGAAGTCTCTAAATCAACAACATCTTCAGAGCACCTACTAT	6360
Qy	6361	TTTGCAGAGCTGTTTAAAGTGTAGTACAGGGCTTTGAGGTTGAGAACTACTGTGGCTAT	6420
Db	6361	TTTGCAGAGCTGTTTAAAGTGTAGTACAGGGCTTTGAGGTTGAGAACTACTGTGGCTAT	6420
Qy	6421	TCTCAGAACCCAAATCTGTAGGGAATGAAATGATAGCAAGTAATAGTTTAAAGAAG	6480
Db	6421	TCTCAGAACCCAAATCTGTAGGGAATGAAATGATAGCAAGTAATAGTTTAAAGAAG	6480
Qy	6481	ACCCCATAGGTCCTTAAACAGCAGCAGGAAGCAAAATGCTTAGGGTGTCAAAGSAAAGAAATG	6540
Db	6481	ACCCCATAGGTCCTTAAACAGCAGCAGGAAGCAAAATGCTTAGGGTGTCAAAGSAAAGAAATG	6540
Qy	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGATCTTCAAGGAGAACTGGATCCA	6600
Db	6541	ATCACATTCAGCTGGGGATCAAGATAGCCTTCTGATCTTCAAGGAGAACTGGATCCA	6600
Qy	6601	TTAGGTCAGGTTGAAGATGATGGAGGCTCACACAGACGGAGCAACCATGCCAAGTAGGA	6660
Db	6601	TTAGGTCAGGTTGAAATGATGGAGGCTCACACAGACGGAGCAACCATGCCAAGTAGGA	6660
Qy	6661	GAGTATAAGGCATCTCTGGGAGATTAGAAATAATTACTGTACCTTAACCTTGAGTTGCCGT	6720
Db	6661	GAGTATAAGGCATCTGGGAGATTAGAAATAATTACTGTACCTTAACCTTGAGTTGCCGT	6720
Qy	6721	AGCTATCACTCACCATTAATGCAATTTCTACCCCTGAACTCTGTGGTGTAGGGAAGA	6780
Db	6721	AGCTATCACTCACCATTAATGCAATTTCTACCCCTGAACTCTGTGGTGTAGGGAAGA	6780
Qy	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGGCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAGACCCAGCTCATACAGAGTCCAAGGGCTTTTGGGATATTGGGTTATGA	6840
Qy	6841	TCACCTGGGGTGTCAATGAGAGATCCCTAAGAAAGGAGGACCAGCATCCCTTATATGGTG	6900
Db	6841	TCACCTGGGGTGTCAATGAGAGATCCCTAAGAAAGGAGGACCAGCATCCCTTATATGGTG	6900
Qy	6901	AATGTGTGTTTAAACAAGTTAGATGAGAGTGTAGGAGACCAAGTTAGAAAGCCCAATAAGCAT	6960
Db	6901	AATGTGTGTTTAAAGAAGTTAGATGAGAGTGTAGATGAGAGACCAAGTTAGAAAGCCCAATAAGCAT	6960
Qy	6961	TTCCAGATGAGAGATAATGTTCTTGAATPCCAAATAGTCCCAAGCTCTAAATGAGATGG	7020
Db	6961	TTCCAGATGAGAGATAATGTTCTTGAATPCCAAATAGTCCCAAGCTCTAAATGAGATGG	7020
Qy	7021	GTGAATGAGGAAATAGGAAGACAGACAGATGGTCCCTAGGTTTGTATGCCT	7080
Db	7021	GTGAATGAGGAAATAGGAAGACAGACAGATGGTCCCTAGGTTTGTATGCCT	7080
Qy	7081	CTTTCCTGGGTCTCTGTCTCCACAGGAGAGGCATGGGGCACTACGCTTTAGCTGAACG	7140

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RESULT 7
AR149461 AR149461 10825 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 5 from patent US 6228594.
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ACCESSION AR149461
VERSION AR149461.1 GI:15114052
KEYWORDS
SOURCE unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10825)
AUTHORS Thomas,W.J., Drayna,D.T., Feder,J.N., Gnirke,A., Ruddy,D.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Method for determining the presence or absence of a hereditary
hemochromatosis gene mutation
JOURNAL Patent: US 6228594-A 5 08-MAY-2001;
FEATURES Location/Qualifiers
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BASE COUNT 2998 a 2252 c 2649 g 2926 t
ORIGIN
Query Match 100.0%; Score 10823; DB 6; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TCTAAGGTTGAGATAAAATTTTTTAAATGTATGATTGAATTTTGAATAATCATAAATATTTA 60
Db 1 TCTAAGGTTGAGATAAAATTTTTTAAATGTATGATTGAAATTTTGAATAATCATAAATATTTA 60
Qy 61 AATATCTAAGTTTCAGATCAGAACATTTGGAAGCTACTTTCCCAATCAACAACACCCCT 120
Db 61 AATATCTAAGTTTCAGATCAGAACATTTGGAAGCTACTTTCCCAATCAACAACACCCCT 120
Qy 121 TCAGGATTTTAAAAACAAGGGGACACTGGATTCACCTAGTGTGTTTCCAGCAGGTACCTT 180
Db 121 TCAGGATTTTAAAAACAAGGGGACACTGGATTCACCTAGTGTGTTTCCAGCAGGTACCTT 180
Qy 181 CTGCTGTAGAGAGAGAGAACTAAAGTCTGAAACCTGTGCTTTTCCACCAGGAAGTT 240
Db 181 CTGCTGTAGAGAGAGAGAACTAAAGTCTGAAACCTGTGCTTTTCCACCAGGAAGTT 240

Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGTCTTTCACCGAGAAATT 240
QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGC 300
Db 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCGC 300
QY 301 TTTCGCCGCCGCCAAAAGACGAGATTTAACGGGACGTGGGCCAGAGCTGGGGAA 360
Db 301 TTTCGCCGCCGCCAAAAGACGAGATTTAACGGGACGTGGGCCAGAGCTGGGGAA 360
QY 361 ATGGGCCCGAGCCAGGCGCGCTTCTCCTGTGATGCTTTTGCAGACCGCGGCTCGT 420
Db 361 ATGGGCCCGAGCCAGGCGCGCTTCTCCTGTGATGCTTTTGCAGACCGCGGCTCGT 420
QY 421 CAGGGCGCTTGCCTGGTGAGTCCAGGGCTGCGGGCGAACTAGGGCGGCGGGGGGTG 480
Db 421 CAGGGCGCTTGCCTGGTGAGTCCAGGGCTGCGGGCGAACTAGGGCGGCGGGGGGTG 480
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540
Db 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTGGGAGTTTGTAACTTTTGGAGGACCTGC 540
QY 541 TCAACCCATCCGCAAGCCCTCTCCCTACTTCTGTGCTCCAGACCCCGTGAGGGAGTGC 600
Db 541 TCAACCCATCCGCAAGCCCTCTCCCTACTTCTGTGCTCCAGACCCCGTGAGGGAGTGC 600
QY 601 CTACCACTCAACTGAGATAGGGTCCCTCGCCCGAGGACCTGCCCTCCCGCGCTGT 660
Db 601 CTACCACTCAACTGAGATAGGGTCCCTCGCCCGAGGACCTGCCCTCCCGCGCTGT 660
QY 661 CCGGCTCTCGGAGTGACTTTTGAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 720
Db 661 CCGGCTCTCGGAGTGACTTTTGAACCGCCCACTCCCTTCCCCCAACTAGAAATGCTTT 720
QY 721 TAAATAAATCTCGTAGTCTTCCACTGAGCTGAGCTAGGCTGGGCTCCTTGAACCTGG 780
Db 721 TAAATAAATCTCGTAGTCTTCCACTGAGCTAGGCTAGGCTGGGCTCCTTGAACCTGG 780
QY 781 AACTCGGGTTTATTTCCAAATGACGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 840
Db 781 AACTCGGGTTTATTTCCAAATGACGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 840
QY 841 AAGTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCAGAGGATCCGACGG 900
Db 841 AAGTCTTCCCTGAGTGTGCGGAGAGGCTGAGCAAAACCCAGAGGATCCGACGG 900
QY 901 GGTTCACCTCAGAACGAATCGTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGGA 960
Db 901 GGTTCACCTCAGAACGAATCGTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGGA 960
QY 961 TCTGAATCTTCCATTCACCCACTTTTGGTGAGACCTGGGTGGAGGCTCTAGGT 1020
Db 961 TCTGAATCTTCCATTCACCCACTTTTGGTGAGACCTGGGTGGAGGCTCTAGGT 1020
QY 1021 GGGAGCTCCTGAGAGGCTTACCTCGGGCTTTCCCGACTTCTGGCAATTTGTTCTTTT 1080
Db 1021 GGGAGCTCCTGAGAGGCTTACCTCGGGCTTTCCCGACTTCTGGCAATTTGTTCTTTT 1080
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Db 1081 GCCTGAAAATTAAGTATATGTTTGTGAACTGTTGAACCTGAACTGAACTGAACTGAACTG 1140
QY 1141 CTAGGCTTATTTGATTTGCAATGTCTGTGTAATTAAGAGCCCTCTFACAAAGTACTGA 1200
Db 1141 CTAGGCTTATTTGATTTGCAATGTCTGTGTAATTAAGAGCCCTCTFACAAAGTACTGA 1200
QY 1201 TAATGAACATGTAAGCAATGCACCTCTCAAGTTACATCATATCATATCATATCATATTTGA 1260
Db 1201 TAATGAACATGTAAGCAATGCACCTCTCAAGTTACATCATATCATATCATATCATATTTGA 1260
QY 1261 TTTTCACTAGGATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320
Db 1261 TTTTCACTAGGATAGGGAGGTAGGAGCTAAATAACGTTTATTTTACTAGAGTTAACT 1320

QY 1321 GGAATTCAGATTATATAACTCTTTTTCAGTTTACAAAGAACATAAATAATCTGTTTTCTG 1380
Db 1321 GGAATTCAGATTATATAACTCTTTTTCAGTTTACAAAGAACATAAATAATCTGTTTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGGCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTTGGCCTGTAG 1440
QY 1441 TGTAGCAGAGTGTCTGTGGGTTCACACCGCGCTCAGCAGCAGCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCAGAGTGTCTGTGGGTTCACACCGCGCTCAGCAGCAGCTTTGAGTTTGGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAATAGAGCATGGCAGCCTGCTTCTCTGG 1560
Db 1501 CTACGTGTATCCACATTTTACACATGACAAATAGAGCATGGCAGCCTGCTTCTCTGG 1560
QY 1561 CAAATTTATTCAGTACTACCTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
Db 1561 CAAATTTATTCAGTACTACCTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATTTCTTAAACATCAGCTGCAATFAGAGTTGAATAATAAATTTCAATGTTGAGCAG 1680
Db 1621 TATGATTTCTTAAACATCAGCTGCAATFAGAGTTGAATAATAAATTTCAATGTTGAGCAG 1680
QY 1681 AAATATTCATTTTACAAGTGAATGAGTCCAGGCACTGTGTCACCTGTTCAAGCCC 1740
Db 1681 AAATATTCATTTTACAAGTGAATGAGTCCAGGCACTGTGTCACCTGTTCAAGCCC 1740
QY 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCTTTTGATATTTTGCAATTTCTAGTGGAGA 1800
Db 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCTTTTGATATTTTGCAATTTCTAGTGGAGA 1800
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Db 1801 GATGACAATAAGCAATGAGCAGAAAGATATACAACTCAGGAAATCATGGGTCTTGA 1860
QY 1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTTGACACTTTGAGCAGAGACATGAAGGA 1920
Db 1861 GAAGCAGAGAGTCAAGGCAAGTCACTCTGGGCTTGACACTTTGAGCAGAGACATGAAGGA 1920
QY 1921 AATAAGATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTTGGCAAG 1980
Db 1921 AATAAGATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTTGGCAAG 1980
QY 1981 TTGGATTTAAAAGCGGGTTTCTCAGCACTACTCATGTTGTGTGTGTGGGGGGGGGG 2040
Db 1981 TTGGATTTAAAAGCGGGTTTCTCAGCACTACTCATGTTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCGTGGGGTGGGAAGGGGACTTACCCTCTGCATGTAGGATCTCTAGCAGTATCCTGT 2100
Db 2041 CGGCGTGGGGTGGGAAGGGGACTTACCCTCTGCATGTAGGATCTCTAGCAGTATCCTGT 2100
QY 2101 CCTCCTACTCACTAGTGTCTAGGAGCACTCCCGAGCTTTTGACAACCAAAATGTCTCT 2160
Db 2101 CCTCCTACTCACTAGTGTCTAGGAGCACTCCCGAGCTTTTGACAACCAAAATGTCTCT 2160
QY 2161 AAATTTGGCCATGTCACCTAGTAGACAAACTCTCTGTTTGAAGAGCTCGGGTTGAAAA 2220
Db 2161 AAATTTGGCCATGTCACCTAGTAGACAAACTCTCTGTTTGAAGAGCTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAAATGGGCTCAGAGAGGA 2280
Db 2221 AATAACAAGTAGTGTGGGAGTAGAGGCCAAGAGTAAATGGGCTCAGAGAGGA 2280
QY 2281 GCCACAAACAGGTTGTGAGGCGCTGTAGGCTGTGTGTGAATTTCTAGCCAAGGAGTA 2340
Db 2281 GCCACAAACAGGTTGTGAGGCGCTGTAGGCTGTGTGTGAATTTCTAGCCAAGGAGTA 2340
QY 2341 ACAGTGTCTGTACAGGCTTTTAAAAGATTTGCTCTGCTGCTATGTGGAAGCAGAGT 2400
Db 2341 ACAGTGTCTGTACAGGCTTTTAAAAGATTTGCTCTGCTGCTATGTGGAAGCAGAGT 2400

Qy	2401	AAGGAGCAACAGTAAAGACAGGAGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2460
Db	2401	AAGGAGCAACAGTAAAGACAGGAGGAGCCAGCCAGGAAGCTGTTACACAGTCCAGGCAAG	2460
Qy	2461	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAGGGAGTGACAAACCATGTCTCCTGAA	2520
Db	2461	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAAGGGAGTGACAAACCATGTCTCCTGAA	2520
Qy	2521	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAGAAATTTGG	2580
Db	2521	TATATTCTGAAGGAAGTTGCTGAAGGATTCTATGTTGTGTGAGAGAAGAAATTTGG	2580
Qy	2581	CTGGGTGTAGTGTATGCTATGCCAAGAGAGAGGCCAAGAGAGACAGATTCTCTGAGCTCAGGA	2640
Db	2581	CTGGGTGTAGTGTATGCTATGCCAAGAGAGAGGCCAAGAGAGACAGATTCTCTGAGCTCAGGA	2640
Qy	2641	GTTCAAGACACAGCCTGGGCAACACAGCAAAAACCCCTCTCTACAAAAAATACAAAAATTA	2700
Db	2641	GTTCAAGACACAGCCTGGGCAACACAGCAAAAACCCCTCTCTACAAAAAATACAAAAATTA	2700
Qy	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCTCTAGCTTACTCTGGGAGGCTGAGGTGAGGGTA	2760
Db	2701	GCTGGGTGTGGTGGCATGCACCTGTGATCTCTAGCTTACTCTGGGAGGCTGAGGTGAGGGTA	2760
Qy	2761	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTTCAGC	2820
Db	2761	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTTCAGC	2820
Qy	2821	CTAGGTGACAGACGAAGACCCCTGCTCCCTGACCCCTGAAAAAGAGAAGTTAAAGT	2880
Db	2821	CTAGGTGACAGACGAAGACCCCTGCTCCCTGACCCCTGAAAAAGAGAAGTTAAAGT	2880
Qy	2881	TGACITTTGCTCTTATTTTAAATTTATTTGGCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
Db	2881	TGACITTTGCTCTTATTTTAAATTTATTTGGCCTGAGCAGTGGGGTAAATTTGGCAATGCCAT	2940
Qy	2941	TTCTGAGATGGTCAAGGCCAGAGGAAGAGCAGTTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Db	2941	TTCTGAGATGGTCAAGGCCAGAGGAAGAGCAGTTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Qy	3001	GGACATGTTAAAGTTTGAGATTCCAGTCCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAAGTTTGAGATTCCAGTCCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Qy	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGCACGGTGGCTCACTCTGTAAATCCCAGCACT	3120
Db	3061	CAGTGTAAAGAAATTCAGGACCAAGGCTGGCACGGTGGCTCACTCTGTAAATCCCAGCACT	3120
Qy	3121	TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTGAGGCTTTGAGACAAAGCTTTGGCCAACTA	3180
Db	3121	TTGGTGGCTGAGCGAGGTAGATCATTTGAGGTGAGGCTTTGAGACAAAGCTTTGGCCAACTA	3180
Qy	3181	TGCTGAAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGTGGCGCAGCCCT	3240
Db	3181	TGCTGAAACCCCATGTCTACTAAAAATACAAAAATTTAGCCTGGTGTGGTGGCGCAGCCCT	3240
Qy	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGTGTAGGAGAAATCCCTTGAAACCCAGGAGGTCCAGG	3300
Db	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGTGTAGGAGAAATCCCTTGAAACCCAGGAGGTCCAGG	3300
Qy	3301	TTCCAGTGTAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Db	3301	TTCCAGTGTAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGAGACTCTGT	3360
Qy	3361	CTCAAAAAAATAAAAAAAAAAAAAAAAAAATACTGAAGGAATTTATTTCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAATAAAAAAAAAAAAAAAAAAATACTGAAGGAATTTATTTCTCAGGATTTGGG	3420
Qy	3421	TCTAAATTTGCCCTGAGCACCAACTCTCTGAGTCTCAACTTACCATTGGCTAGACACACCTTAAC	3480
Db	3421	TCTAAATTTGCCCTGAGCACCAACTCTCTGAGTCTCAACTTACCATTGGCTAGACACACCTTAAC	3480
Qy	3481	ATTTTCTAGAAATCCACACAGCTTTAGTGGAGTCTGTCTAAATCATCAGTATTGTGAATAGGAT	3540

[illegible]

Db 4561 AGTTGCAGGCGACGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCTC 4620
QY TCCAAATTTCTGGGAAGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTTAGATGTA 4680
Db TCCAAATTTCTGGGAAGGACTTCTCAATCCCTAGAGTCTCTACCTTATAATTTAGATGTA 4680
QY TGAGACAGCCACAAGTCATGGGTTAAATTTCTTTCTCCATGCATATAGGCTCAAAAGGAA 4740
Db TGAGACAGCCACAAGTCATGGGTTAAATTTCTTTCTCCATGCATATAGGCTCAAAAGGAA 4740
QY GTCTCTATGGCCCTTCTCTTTTATTTAAACCAATAATCTTTTGTATATATACCTGTAA 4800
Db GTCTCTATGGCCCTTCTCTTTTATTTAAACCAATAATCTTTTGTATATATACCTGTAA 4800
QY AAATTCAGAAATGTCAAGCGCGGCGACGGTGGCTCACCCCTGTAAATCCCGACACTTTGGG 4860
Db AAATTCAGAAATGTCAAGCGCGGCGACGGTGGCTCACCCCTGTAAATCCCGACACTTTGGG 4860
QY AGGCCAGGCGGTGGTGTCAAGAGTCAGGAGTTTCAGACCCAGCCTGACCAACATGGTGAA 4920
Db AGGCCAGGCGGTGGTGTCAAGAGTCAGGAGTTTCAGACCCAGCCTGACCAACATGGTGAA 4920
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Db ACCCGTCTCTAAAAAATACAAAAATAGCTGGTCACAGTCAATGCGCACCTGTAGTCCCA 4980
QY GCTAATTTGAAGGCTGAGCGAGGCGATCGCTTGAACCTGGGAAGCGAAGTTGCACATGA 5040
Db GCTAATTTGAAGGCTGAGCGAGGCGATCGCTTGAACCTGGGAAGCGAAGTTGCACATGA 5040
QY GCCAAGATCGCGCACTGCACCTCCAGCTTAGCGACGAGTGAGACTCCATCTTAAAAAA 5100
Db GCCAAGATCGCGCACTGCACCTCCAGCTTAGCGACGAGTGAGACTCCATCTTAAAAAA 5100
QY AAAAAAAGGAGAGATTCAGAGATCTCAGCTATCATATGAATACAGGACAAA 5160
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Db ATATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGGTTAAAAAGTTCTTTTCAT 5220
QY AGACATAGCAATTAATCACTGAGCTACCTATCTTACAGTCCGCTTCTTATATCAATATGC 5280
Db AGACATAGCAATTAATCACTGAGCTACCTATCTTACAGTCCGCTTCTTATATCAATATGC 5280
QY CTCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCAATTTCAATGCACATAA 5340
Db CTCTAGGTTGACCCAGGTGAACCTGACCATCTGTATTCAATCAATTTCAATGCACATAA 5340
QY AGGCAATTTTATCTATCAGAACAAAGACATGGGTACAGATATGTATATTACATGTG 5400
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QY AGGAAACAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTAGAGTCCAAATCTTAGG 5460
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QY ACACAAATGGTGTCTCTCTGCTAGCTGTGTTTTTCTGAAAAGGATATTTCTTCCTCC 5520
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Db AACCTATAGAAGGAAGTGAAGTTCAGTCTTCCCTGGCAAGGTAACACAGATCCCTCTC 5580
QY CTATCCTCTCTCTCTCTGTCAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACC 5640
Db CTATCCTCTCTCTCTCTGTCAGTGCCTCTTTGGTGAAGGTGACACATCATGTGACC 5640
QY TCTTCAGTGACCACTCTACGGGTCTCGGGCTTTGAACCTACTACCCCGACCAATCACCATG 5700
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Db AAGTGGCTCAAGATAAGCAGCAATGGATGCCAAGGAGTTTCAAGACCTAAAGACGTATTG 5760
QY CCCAATGGGATGGGACCTTACCAGGCTGGATAACCTTTGGCTGTACCCCTTGGGGAAGAG 5820
Db CCCAATGGGATGGGACCTTACCAGGCTGGATAACCTTTGGCTGTACCCCTTGGGGAAGAG 5820
QY CAGAGATATACGTTNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG 5880
Db CAGAGATATACGTTNCCAGGTGGAGCACCCAGGCTTGGATCAGCCCTCATTTGTGATCTGG 5880
QY GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGCC 5940
Db GGTATGTGACTGATGAGACCCAGGAGCTGAGAAAATCTATTGGGGGTTGAGAGAGTGCC 5940
QY TGAGGAGGTAAATATATGGCAGTGAGATGAGATCTGCTCTTTAGGGGTTGGGCTGAGG 6000
Db TGAGGAGGTAAATATATGGCAGTGAGATGAGATCTGCTCTTTAGGGGTTGGGCTGAGG 6000
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Db GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTTTTAGAGCCCTCACCGTCTGGCACCC 6060
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Db TACTCATTTGAGTCATCAGTGGAAATGCTGTTTTTGTGCTCATCTTGTTCATTGGAATTT 6120
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Db TAGTACTCTGCCCCAGGCACAGTGGGAAGAGGSCAGAGGGATCTGGCATCCATGGG 6240
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Db AAGCATTTTCTCATTTATATTTCTTTGGGACACCAAGCAGCTCCCTGGGACACAGAAAT 6300
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Db GAGTATAAGGCATCTGGGAGATTAGAAATATTTACTGTACCTTAACCTGAGTTTGGGT 6720
QY AGCTATCACTCACCAATTTATGCAATTTCTACCCCTGAAACATCTGTGGTGAAGGAAAAGA 6780
Db AGCTATCACTCACCAATTTATGCAATTTCTACCCCTGAAACATCTGTGGTGAAGGAAAAGA 6780

Qy 6781 GAATCAGAAAGCCAGCTCATACAGAGTCCAAAGGCTCTTTGGGATATGGGTTATGA 6840
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 Db 7921 TCCACACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTCTCTGATAATGAAA 7980
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 Qy 8161 AGCACTTTGGGAGGCCAAAGCGGTGGATCAGGAGGTGAGGATCAGAGATCAGAGCACTCCTGGC 8220
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 Db 8221 TAACATGGTGAACCCCATCTCTAATAAAAAACAAAAATTAGCTGGCGGTGGTGGCAG 8280
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 Db 8281 AGCCCTGTAGTCCCAGCTACTCGGAAGGTGAGGAGGAGAAATGCGCATGAACCCAGGAGG 8340
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 Db 8701 CCTGAAGAAAGTCCCTGGAATGTGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8760
 Qy 8761 TTTCTTTGGACCCCTACGCAAGGACTGTAATTTGTTGGGACAGCTAGTGGCCCTGCTGGCG 8820
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 Db 8821 TTCACACAGCTGCTCCCTAGCCAGTCCCTCTGAGTGGGACAGCTAGTGGCCCTGCTGGCG 8880
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 Db 8881 CCTCAATGAAGTGGAGTAACTCTCTCAATTTGAGATGGTATTAATGGAAGCCACCAAGTG 8940
 Qy 8941 GCTTAGAGATGCCAGGCTCTTCCATGGAGCCACTGGGGTCCGGGTGCACATTTAAAAA 9000

BASE COUNT 2999 a 2252 c 2648 g 2926 t									
ORIGIN									
Query Match 100.0%; Score 10823; DB 6; Length 10825;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1	TCTAAGTTGAGATAAAATTTTAAATGTATGATGTAATTTTGAATATCATATAATATTTA	60						
Db	1	TCTAAGTTGAGATAAAATTTTAAATGTATGATGTAATTTTGAATATCATATAATATTTA	60						
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Db	61	AATATCTAAAGTTCAGATCAGAACTTGCAGAGCTACTTTCCCAATCAACAACACCCCT	120						
Qy	121	TCAGATTTTAAACCAAGGGGGACACTGGATCACCTAGTAGTGTTCACAAGCAGGTACCTT	180						
Db	121	TCAGATTTTAAACCAAGGGGGACACTGGATCACCTAGTAGTGTTCACAAGCAGGTACCTT	180						
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTCCTTTTCAACAGGAAGTT	240						
Db	181	CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTTCCTTTTCACCGAAGTT	240						
Qy	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTCTTGGAGCCATCCCG	300						
Db	241	TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTCTTGGAGCCATCCCG	300						
Qy	301	TTTCCCCCCCCCAAAAGAGCGGAGATTTAACGGGGACGTGCGCCAGAGCTGGGGAA	360						
Db	301	TTTCCCCCCCCCAAAAGAGCGGAGATTTAACGGGGACGTGCGCCAGAGCTGGGGAA	360						
Qy	361	ATGGCCCGCGAGCAGCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGTCTG	420						
Db	361	ATGGCCCGCGAGCAGCGCGCTTCTCCTCTGATGCTTTTGCAGACCGCGTCTG	420						
Qy	421	CAGGGCGCTTGCTCGGTAGTCCAGGGCTGCGGGCGAATAGGGCGCGCGGGGTG	480						
Db	421	CAGGGCGCTTGCTCGGTAGTCCAGGGCTGCGGGCGAATAGGGCGCGCGGGGTG	480						
Qy	481	GAATAATCGAACTAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGGAGGACCTGC	540						
Db	481	GAATAATCGAACTAGCTTTTCTTGGCTTGGAGTTGCTAACTTTGGAGGACCTGC	540						
Qy	541	TCAACCCATTCCGCAAGCCCTCTCCCTACTTTCTGCTTCCAGACCCCGTGAGGAGTGC	600						
Db	541	TCAACCCATTCCGCAAGCCCTCTCCCTACTTTCTGCTTCCAGACCCCGTGAGGAGTGC	600						
Qy	601	CTACCACTGAATGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT	660						
Db	601	CTACCACTGAATGCAGATAGGGTCCCTCGCCCGCAGGACCTGCCCCCTCCCGGCTGT	660						
Qy	661	CCGGCTCTGCGAGTGACTTTTGAACCGCCACTCCCTTCCCCCACTAGAATGCTTT	720						
Db	661	CCGGCTCTGCGAGTGACTTTTGAACCGCCACTCCCTTCCCCCACTAGAATGCTTT	720						
Qy	721	TAAATAATCTCGTAGTTCCTCACTTGAAGCTGAGCTTGGAGCTTGGACCTGG	780						
Db	721	TAAATAATCTCGTAGTTCCTCACTTGAAGCTGAGCTTGGAGCTTGGACCTGG	780						
Qy	781	AACCTCGGTTTATTTCCCAATGTACGTGTGCAGTTTTCCTCCAGTCAATCTCCAAACAGG	840						
Db	781	AACCTCGGTTTATTTCCCAATGTACGTGTGCAGTTTTCCTCCAGTCAATCTCCAAACAGG	840						
Qy	841	AAGTTCTTCCCTGAGTGTTCGCGAGAAGGCTGAGCAAAACCCACAGAGGATCCGACGG	900						
Db	841	AAGTTCTTCCCTGAGTGTTCGCGAGAAGGCTGAGCAAAACCCACAGAGGATCCGACGG	900						
Qy	901	GGTTTCCACCTCAGACGAATGCGTTTGGCGGTGGGGCGCGAAGAGTGGGTTGGGA	960						
Db	901	GGTTTCCACCTCAGACGAATGCGTTTGGCGGTGGGGCGCGAAGAGTGGGTTGGGA	960						
Qy	961	TCTGAATTTCTTCCACCTTCCACCCACTTTTGGTGTAGACCTTGGGGTGTCTAGGGT	1020						

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Db 2101 CCTCCCTACTACTAGGTGCTAGGAGCACTCCCCAGTCTTGACACCAAAAATGTCTCT 2160
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1 (bases 1 to 246240)
AUTHORS Feder, J. Nathan., Kromal, G. Scott., Lauer, P. M., Ruddy, D. A.,
Thomas, W., Tsuchihashi, Z. and Wolff, R. K.
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JOURNAL Patent: US 5872237-A 21 FEB-1999;
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DB	201904	ACGCTCATTTGTAAGAAAGCTATAAAATGAATACAATTAAGCTGTTATTTAATTAGCCAG	201963
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ACCESSION AR036574
VERSION AR036574.1 GI:5953242
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 246240)
FEDER,J.Nathan., Kronmal,G.Scott., Lauer,P.M., Ruddy,D.A.,
Thomas,W., Tsuchihashi,Z. and Wolff,R.K.
Megabase transcript map: novel sequences and antibodies thereto
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Location/Qualifiers
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Db 201484 AGTAGCTGGGATTACAGCGGTGCACCACTGCTCCGGCTAAATTTTGTATTTTAGTAGA 201543
Qy 9241 GACAGGTTTTACCATGTTGGCCAGGCTGCTCTCGAACTCTCCTGACCTCGTATCCGCC 9300
Db 201544 GACAGGTTTTACCATGTTGGCCAGGCTGCTCTCGAACTCTCCTGACCTCGTATCCGCC 201603
Qy 9301 TGCTCGGCTCCCAAGTGTCTGAGATTACAGGTGTGAGCCACCTGCCAGCCGCTCAA 9360
Db 201604 TGCTCGGCTCCCAAGTGTCTGAGATTACAGGTGTGAGCCACCTGCCAGCCGCTCAA 201663
Qy 9361 AGAGCTTAATATATATATATCCAGATGCACTGTGTACTTTACTTACTACTACATGCATG 9420
Db 201664 AGAGCTTAATATATATATCCAGATGCACTGTGTACTTTACTTACTACTACATGCATG 201723
Qy 9421 GCTGCATAAATGGGTCAAGCATCTCTTGAAGGCGAGGTGCTTCAGGATACCATAT 9480
Db 201724 GCTGCATAAATGGGTCAAGCATCTCTTGAAGGCGAGGTGCTTCAGGATACCATAT 201783
Qy 9481 ACAGCTCAGAGTTTCTTCTTAGGCATTAATTTTAGCAAAAGATATCTCATCTCTCTT 9540
Db 201784 ACAGCTCAGAGTTTCTTCTTAGGCATTAATTTTAGCAAAAGATATCTCATCTCTCTT 201843
Qy 9541 TTAACACATTTCTTTTTTTTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Db 201844 TTAACACATTTCTTTTTTTTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 201903
Qy 9601 ACGTCAATGTAGAAAAGCTATAAAATGAATACAAATTAAGCTGTATTTAAATAGCCAG 9660
Db 201904 ACGTCAATGTAGAAAAGCTATAAAATGAATACAAATTAAGCTGTATTTAAATAGCCAG 201963
Qy 9661 TGAAAACTATTACAACTTGTCTATTACCTGTGTAGTATTATTGTCGCAATTAATAATGCA 9720
Db 201964 TGAAAACTATTACAACTTGTCTATTACCTGTGTAGTATTATTGTCGCAATTAATAATGCA 202023
Qy 9721 TATACTTTAATAAATGTATATTGTATTGATACCTGCAATTTTATGAAAGTCTCTGTTTC 9780
Db 202024 TATACTTTAATAAATGTATATTGTATTGATACCTGCAATTTTATGAAAGTCTCTGTTTC 202083
Qy 9781 ATCTTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTTTCCITCTTAATTT 9840
Db 202084 ATCTTGTATATACTTAATCGCTTTGTCATTTTGGAGACATTTATTTTCTCTTAATTT 202143
Qy 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGTGGTCCGCAATTAATCGTGT 9900
Db 202144 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGTGGTCCGCAATTAATCGTGT 202203
|||||

[illegible]

QY	3897	GA	CTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCACGCTGAGTCACAGTC	3955
DB	4787	GA	CTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCACGCTGAGTCACAGTC	4846
QY	3957	TG	AAAGGGTGGGATCACATGTTTCAGTCTTGACTTCTGGACATATTTATGGAAAAATCAACAAC	4016
DB	4847	TG	AAAGGGTGGGATCACATGTTTCAGTCTTGACTTCTGGACATATTTATGGAAAAATCAACAAC	4906
QY	4017	AC	AGCAAGGGTATGTGGAGAGGGGCCCTACCTTCCTTGAGGTTGTCACAGACTTTTCATCT	4076
DB	4907	AC	AGCAAGGGTATGTGGAGAGGGGCCCTACCTTCCTTGAGGTTGTCACAGACTTTTCATCT	4966
QY	4077	TT	TATGTCATCTTTGAAGGAAACAGCTGGAAGTCTGAGCTCTGTGGCAGCAGGAAGAGG	4136
DB	4967	TT	TATGTCATCTTTGAAGGAAACAGCTGGAAGTCTGAGCTCTGTGGCAGCAGGAAGAGG	5026
QY	4137	GA	AGGAATTTGCTTCCTGAGATCATTTGGTCTTGCGGATGGTGGAATTAGGACCTATT	4196
DB	5027	GA	AGGAATTTGCTTCCTGAGATCATTTGGTCTTGCGGATGGTGGAATTAGGACCTATT	5086
QY	4197	CT	TTTGGTTGTCAGTTAAACAAGGCTGGGATTTTCCAGAGTCCACACCCCTGCAGGTCTAT	4256
DB	5087	CT	TTTGGTTGTCAGTTAAACAAGGCTGGGATTTTCCAGAGTCCACACCCCTGCAGGTCTAT	5146
QY	4257	CT	TGGGCTGTGAAATGCAAGAGACAACAGTACCGAGGGCTACTGGAAGTACCGGTATGA	4316
DB	5147	CT	TGGGCTGTGAAATGCAAGAGACAACAGTACCGAGGGCTACTGGAAGTACCGGTATGA	5206
QY	4317	TG	GCAGGACCACTTGTAATTCCTGCCCTGCACACTTGGATTTGGAGACGACGAAACCCAG	4376
DB	5207	TG	GCAGGACCACTTGTAATTCCTGCCCTGCACACTTGGATTTGGAGACGACGAAACCCAG	5266
QY	4377	GG	CTGGCCCCACCAAGCTGAGTGGGAAGGCACAAGATTCGGGCCAGGCAGAACAGGC	4436
DB	5267	GG	CTGGCCCCACCAAGCTGAGTGGGAAGGCACAAGATTCGGGCCAGGCAGAACAGGC	5326
QY	4437	CT	ACTTGGAGAGGAGTGCCTTCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGTGT	4496
DB	5327	CT	ACTTGGAGAGGAGTGCCTTCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGTGT	5386
QY	4497	TT	TGGACCAACAAGGTATGGTGGAAACACATTCCTGCCCTTACTCTAGTGGCAGAGTG	4556
DB	5387	TT	TGGACCAACAAGGTATGGTGGAAACACATTCCTGCCCTTACTCTAGTGGCAGAGTG	5446
QY	4557	GAG	AGGTTGCAGGGCACGGAAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTG	4616
DB	5447	GAG	AGGTTGCAGGGCACGGAAATCCCTGGTGGAGTTTCAGAGTGGCTGAGGCTGTGTG	5506
QY	4617	CT	CTCCAAATCTGGGAAGGACTTCTCAATCCTACAGTCTCTACTTATATTCAGA	4676
DB	5507	CT	CTCCAAATCTGGGAAGGACTTCTCAATCCTACAGTCTCTACTTATATTCAGA	5566
QY	4677	TG	TATGAGACAGCCACAAGTCATGGGTTTAAATTCCTTTCTCCATGCATATGGCTCAAG	4736
DB	5567	TG	TATGAGACAGCCACAAGTCATGGGTTTAAATTCCTTTCTCCATGCATATGGCTCAAG	5626
QY	4737	GG	AGTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTGTATATTTATACCTG	4796
DB	5627	GG	AGTGTCTATGGCCCTTGCTTTTATTTAACCAATAATCTTTGTATATTTATACCTG	5686
QY	4797	TT	AAAAATTCAGAAATGTCAAGCCGGGACGGTGGCTCACCCCTGTAAATCCACGACTT	4856
DB	5687	TT	AAAAATTCAGAAATGTCAAGCCGGGACGGTGGCTCACCCCTGTAAATCCACGACTT	5746
QY	4857	TG	GAGGCCGAGCGGGTGTGCACAGGTCAGGAGTTTGGACACAGCCTGACCAACATGG	4916
DB	5747	TG	GAGGCCGAGCGGGTGTGCACAGGTCAGGAGTTTGGACACAGCCTGACCAACATGG	5806
QY	4917	TG	AACCCGTCTCTAAAAAATAACAAAAATATAGCTGGTCACAGTCATGCGCACTGTAGT	4976
DB	5807	TG	AACCCGTCTCTAAAAAATAACAAAAATATAGCTGGTCACAGTCATGCGCACTGTAGT	5866

Qy	4377	CCAGCTAATTGGAAGCGCTGAGCGCAGGAGCATCGCTTGAACTTGGGAAGCGGAAGTTGCA	5036
Db	5867	CCAGAGTAAATTGGAAGCGCTGAGCGCAGGAGCATCGCTTGAACTTGGGAAGCGGAAGTTGCA	5926
Qy	5037	CTGAGCCACAGATCGCGCCACTGCATCTCCAGCCTTAGCGACGACAGGTGAGACTTCCATCTTAA	5096
Db	5927	CTGAGCCACAGATCGCGCCACTGCATCTCCAGCCTTAGCGACGACAGGTGAGACTTCCATCTTAA	5984
Qy	5097	AAAAAATAATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGGTTTAAAGCTTTCCT	5156
Db	5985	AAAAAATAATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGGTTTAAAGCTTTCCT	6044
Qy	5157	CAAAATATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGGTTTAAAGCTTTCCT	5216
Db	6045	CAAAATATCAAGTGAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGGTTTAAAGCTTTCCT	6104
Qy	5217	TCATAGAACATAGCAATATATCACTAGAGTACCTATCTTACAAGTCGCGTCTTATATACA	5276
Db	6105	TCATAGAACATAGCAATATATCACTAGAGTACCTATCTTACAAGTCGCGTCTTATATACA	6164
Qy	5277	ATGCCTCCTAGGTGACCCAGGTGAACTGACCTCTGATTTCAATCATATTTTCAATGCAC	5336
Db	6165	ATGCCTCCTAGGTGACCCAGGTGAACTGACCTCTGATTTCAATCATATTTTCAATGCAC	6224
Qy	5337	ATAAGGGCAATTTATCTATCAGACAAAGAACATGGTAAACAGATATGTATATTTACA	5396
Db	6225	ATAAGGGCAATTTATCTATCAGACAAAGAACATGGTAAACAGATATGTATATTTACA	6284
Qy	5397	TGTGAGGAGAACAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTTAGAGTCCAAATCT	5456
Db	6285	TGTGAGGAGAACAGCTGATCTGACTGCTCTCCAAAGTGACACTGTGTTAGAGTCCAAATCT	6344
Qy	5457	TAGGACACAAATGGTGTCCTCTCTAGCTGTTTTTTTTCTGAAAGGGTATTTTCTCTC	5516
Db	6345	TAGGACACAAATGGTGTCCTCTCTAGCTGTTTTTTTTCTGAAAGGGTATTTTCTCTC	6404
Qy	5517	CTCCAACTATAGAAGGAAGTGAAGTTCAGATCTCTCTGCGCAGGGTAAACAGATCCCC	5576
Db	6405	CTCCAACTATAGAAGGAAGTGAAGTTCAGATCTCTCTGCGCAGGGTAAACAGATCCCC	6464
Qy	5577	TCTCCTCATCTTCTCTCTTCTCTCTCAAGTCGCTCTTGGTGAAGGTGACACATCATGT	5636
Db	6465	TCTCCTCATCTTCTCTCTTCTCTCTCAAGTCGCTCTTGGTGAAGGTGACACATCATGT	6524
Qy	5637	GACCTCTTCACTGACACACTCTACGGTGTGCGGCTTGAACTACTACCCCAAGACATCAC	5696
Db	6525	GACCTCTTCACTGACACACTCTACGGTGTGCGGCTTGAACTACTACCCCAAGACATCAC	6584
Qy	5697	CATGAAGTGGCTCAAGGATAAGCAGCAATGGATGCCAAGGATTCGAACCTTAAGACGT	5756
Db	6585	CATGAAGTGGCTCAAGGATAAGCAGCAATGGATGCCAAGGATTCGAACCTTAAGACGT	6644
Qy	5757	ATTGCCAATGGGGATGGGACCTACACAGGGCTGGATTAACCTTGCGCTGTAACCCCTGGGGA	5816
Db	6645	ATTGCCAATGGGGATGGGACCTACACAGGGCTGGATTAACCTTGCGCTGTAACCCCTGGGGA	6704
Qy	5817	AGACACAGATATACGTTCACAGGTGAGCACCACAGGCTTGGATCAGCCCTCATTTGTTGAT	5876
Db	6705	AGACACAGATATACGTTCACAGGTGAGCACCACAGGCTTGGATCAGCCCTCATTTGTTGAT	6764
Qy	5877	CTGGGGTATGTGACTGATGAGACCCAGGAGCTGAGAAATCTATTGCGGGTGTGAGAGGAG	5936
Db	6765	CTGGGGTATGTGACTGATGAGACCCAGGAGCTGAGAAATCTATTGCGGGTGTGAGAGGAG	6824
Qy	5937	TGCTCTGAGGAGGTAAATTATGGCAGTCCAGATGAGGATCTGCTCTTTGTTAGGGGTGGGCT	5996
Db	6825	TGCTCTGAGGAGGTAAATTATGGCAGTCCAGATGAGGATCTGCTCTTTGTTAGGGGTGGGCT	6884
Qy	5997	GAGGTCGCAATCAAGGCTTTTAACCTTGCTTTTCTGTTTATAGACCTCTACCGTCTGGC	6056
Db	6885	GAGGTCGCAATCAAGGCTTTTAACCTTGCTTTTCTGTTTATAGACCTCTACCGTCTGGC	6944
Qy	6057	ACCCTAGTCAATTGGGAGTCATCAGTGGAAATTGCTGTTTTTGTTCGTCATCTGTGTTCAATGGA	6116

Db 6945 ACCGTAGTCATTGGAGTCATCAGTGGNAATTCGTGTTTTGTCGTCATCTGTTTCATTGGA 7004
 QY 6117 ATTTGTTTCATAATATTAAGGAAGAGCGAGGGTTCAAGTAGTAGGAACAAGGGGAAGT 6176
 Db 7005 ATTTGTTTCATAATATTAAGGAAGAGCGAGGGTTCAAGTAGTAGGAACAAGGGGAAGT 7064
 QY 6177 CTCTTAGTACTCTGCCAGGSCACAGTGGGAAGGGGSCAGAGGGGATCTGGCATCCA 6236
 Db 7065 CTCTTAGTACTCTGCCAGGSCACAGTGGGAAGGGGSCAGAGGGGATCTGGCATCCA 7124
 QY 6237 TGGGAAGCAATTTTCTCATTTATATTTCTTTGGGACACACAGAGCTCCCTGGGAGACAGA 6296
 Db 7125 TGGGAAGCAATTTTCTCATTTATATTTCTTTGGGACACACAGAGCTCCCTGGGAGACAGA 7184
 QY 6297 AAATAATAGTGTCTCCAGAGATGAAAGTCTCTAATCAACAACATCTTCAGAGACCTA 6356
 Db 7185 AAATAATAGTGTCTCCAGAGATGAAAGTCTCTAATCAACAACATCTTCAGAGACCTA 7244
 QY 6357 CTATTTTGCAGAGCTGTTTAAAGTAGTACAGAGGGCTTTGAGGTTGAGAAAGTCACTGTGG 6416
 Db 7245 CTATTTTGCAGAGCTGTTTAAAGTAGTACAGAGGGCTTTGAGGTTGAGAAAGTCACTGTGG 7304
 QY 6417 CTATTTCTCAGAACCCAAATCTGGTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAA 6476
 Db 7305 CTATTTCTCAGAACCCAAATCTGGTAGGGAATGAAATTTGATAGCAAGTAAATGTAGTTAAA 7364
 QY 6477 GAAGACCCCATGAGGTCCTTAAAGCAGCAGCAAGCAAAATGCTTAGGGTGTCAAAGGAAAG 6536
 Db 7365 GAAGACCCCATGAGGTCCTTAAAGCAGCAGCAAGCAAAATGCTTAGGGTGTCAAAGGAAAG 7424
 QY 6537 AATGATCACATTCAGCTGGGATCAAGATAGCCCTTCTGGATCTTGAAGAGAGAGCTGGAT 6596
 Db 7425 AATGATCACATTCAGCTGGGATCAAGATAGCCCTTCTGGATCTTGAAGAGAGAGCTGGAT 7484
 QY 6597 TCCATAGCTAGGTTGAGATGATGGAGTCTACACAGCGGAGCAACCATGCCAAGT 6656
 Db 7485 TCCATAGCTAGGTTGAGATGATGGAGTCTACACAGCGGAGCAACCATGCCAAGT 7544
 QY 6657 AGGAGATATTAAGGCATACCTGGGAGATAGAAATTAATTAAGTACCTTAACCCCTGAGTTT 6716
 Db 7545 AGGAGATATTAAGGCATACCTGGGAGATAGAAATTAATTAAGTACCTTAACCCCTGAGTTT 7604
 QY 6717 GCGTAGCTATCACTCACCATAATTTGCAATTTCTACCCCTGAACATCTGCTGGTAGGGAA 6776
 Db 7605 GCTTAGCTATCACTCACCATAATTTGCAATTTCTACCCCTGAACATCTGCTGGTAGGGAA 7664
 QY 6777 AAGAAATCAGAAAGACAGCTCATACAGATCCAAAGGCTCTTTTGGGATATTGGGTT 6836
 Db 7665 AAGAAATCAGAAAGACAGCTCATACAGATCCAAAGGCTCTTTTGGGATATTGGGTT 7724
 QY 6837 ATGATCACTGGGTTGTCATTGAAGATCCTTAAGAAAGGAGGACACGATCTCCCTTATAT 6896
 Db 7725 ATGATCACTGGGTTGTCATTGAAGATCCTTAAGAAAGGAGGACACGATCTCCCTTATAT 7784
 QY 6897 GGTGAATGTTGTTTAAAGATTTAGATGAGGTTGAGGAGCCAGTGTAGAAGGCCAATAA 6956
 Db 7785 GGTGAATGTTGTTTAAAGATTTAGATGAGGTTGAGGAGCCAGTGTAGAAGGCCAATAA 7844
 QY 6957 GCATTTCCAGATGAGAGATAATGTTGTTTGAATCCAAATAGTGCCAGGCTTAAATTGAG 7016
 Db 7845 GCATTTCCAGATGAGAGATAATGTTGTTTGAATCCAAATAGTGCCAGGCTTAAATTGAG 7904
 QY 7017 ATGGGTGAATGAGGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGGCTAGGTTGTGAT 7076
 Db 7905 ATGGGTGAATGAGGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGGCTAGGTTGTGAT 7964
 QY 7077 GCTCTTTCTGGTCTCTTGTCTCCACAGGAGGAGCCATGGGCACTACGCTTTAGCTG 7136
 Db 7965 GCTCTTTCTGGTCTCTTGTCTCCACAGGAGGAGCCATGGGCACTACGCTTTAGCTG 8024
 QY 7137 AACGTGAGTGACACGAGCCTGCAGACTCACTGTGGGAGGAGACAAATAGAGACTCA 7196

Db 8025 AACGTGAGTGACACGACGCCCTGCAGACTCACTGTGGGAGGAGACAAAATAGAGACTCA 8084
 QY 7197 AAGAGGGAGTGCAATTTATGAGCTCTTTCATGTTTCAGAGAGAGAGTTGAACCTTAAACATAGA 7256
 Db 8085 AAGAGGGAGTGCAATTTATGAGCTCTTTCATGTTTCAGAGAGAGAGTTGAACCTTAAACATAGA 8144
 QY 7257 AATTGCCCTGACGAACCTCCTTGATTTTAGCCTTCTCTGTTTCAATTTCCCTCAAAAAGATTTC 7316
 Db 8145 AATTGCCCTGACGAACCTCCTTGATTTTAGCCTTCTCTGTTTCAATTTCCCTCAAAAAGATTTC 8204
 QY 7317 CCATTTAGGTTTCTCAGTTTCCCTGCAATGCCGTGATCCCTAGCTGTGACCTCTCCCTCGGA 7376
 Db 8205 CCATTTAGGTTTCTCAGTTTCCCTGCAATGCCGTGATCCCTAGCTGTGACCTCTCCCTCGGA 8264
 QY 7377 ACTGTCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCTCCGTCACCTC 7436
 Db 8265 ACTGTCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCTCCGTCACCTC 8324
 QY 7437 AGAGACATACACTATGTCATTTTCAATTTTCCATTTTGGAAAGGAGCTTCTTAAATTTGG 7496
 Db 8325 AGAGACATACACTATGTCATTTTCAATTTTCCATTTTGGAAAGGAGCTTCTTAAATTTGG 8384
 QY 7497 GGGACTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTTGAACCTGGAGCTGGCTAG 7556
 Db 8385 GGGACTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTTGAACCTGGAGCTGGCTAG 8444
 QY 7557 TCATAACCTTACAGATTTTACATGATATCTATGCAATTTTCTGGACCCGTTCAACTTT 7616
 Db 8445 TCATAACCTTACAGATTTTACATGATATCTATGCAATTTTCTGGACCCGTTCAACTTT 8504
 QY 7617 TCCTTTGAATCCTCTCTGTTTACCCAGTAACCTCATCTGTCAACAAAGCTTTGGGGATT 7676
 Db 8505 TCCTTTGAATCCTCTCTGTTTACCCAGTAACCTCATCTGTCAACAAAGCTTTGGGGATT 8564
 QY 7677 CTTCCATCTGATTTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCAGCAATGGA 7736
 Db 8565 CTTCCATCTGATTTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCAGCAATGGA 8624
 QY 7737 AGAGGCACCTGCCCCAGAAAAGCATATGCTGTGGGTAGTATGATGGGTGTTTT 7796
 Db 8625 AGAGGCACCTGCCCCAGAAAAGCATATGCTGTGGGTAGTATGATGGGTGTTTT 8684
 QY 7797 TAGCAGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGTTGTTTTCTAATTTGGC 7856
 Db 8685 TAGCAGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGTTGTTTTCTAATTTGGC 8744
 QY 7857 ATGAAGGTGTACATACAGATTTGCAAAAGTTTAAAGTTCATTTGGGCTTCAATTTGGGATGCTACTCTA 7916
 Db 8745 ATGAAGGTGTACATACAGATTTGCAAAAGTTTAAAGTTCATTTGGGCTTCAATTTGGGATGCTACTCTA 8804
 QY 7917 GTATTTCCAGACCTGAAGAATCAACAATAATTTCTACCTGCTCTCTCTCTCTCTCTCTGATAAT 7976
 Db 8805 GTATTTCCAGACCTGAAGAATCAACAATAATTTCTACCTGCTCTCTCTCTCTCTCTGATAAT 8864
 QY 7977 GAAAAATATGATAGGATGATAAAAGCACTTACTTGGTCCGACCTTCTTGAGCACCTA 8036
 Db 8865 GAAAAATATGATAGGATGATAAAAGCACTTACTTGGTCCGACCTTCTTGAGCACCTA 8924
 QY 8037 CTTACATGCAATTAAGTGCATCTTCTTACAATAATTTCTATGAGATAGTACTTATTTATCC 8096
 Db 8925 CTTACATGCAATTAAGTGCATCTTCTTACAATAATTTCTATGAGATAGTACTTATTTATCC 8984
 QY 8097 CCATTTCTTTTTTAAATGAAGAAAGTGAAGTAGCGGGGACCGGTGGCTCACCCCTGTAA 8156
 Db 8985 CCATTTCTTTTTTAAATGAAGAAAGTGAAGTAGCGGGGACCGGTGGCTCACCCCTGTAA 9044
 QY 8157 TCCAGACACTTTTGGGAGCCCAAGCGGTTGGATCAGAGGTCAGGAGATCGAGACCATCC 8216
 Db 9045 TCCAGACACTTTTGGGAGCCCAAGCGGTTGGATCAGAGGTCAGGAGATCGAGACCATCC 9104
 QY 8217 TGGCTAAATGGGTGAAACCCCATCTCTTAATAAAAAATACAAAAAATAGCTGGCGTGGT 8276
 Db 9105 TGGCTAAATGGGTGAAACCCCATCTCTTAATAAAAAATACAAAAAATAGCTGGCGTGGT 9164

[illegible]

QY	9357	CAAAAGAGCTTTAAATATATATATACAGATGGCATGTTTACTTTATGTACTACATGCA	9416
Db	10245	CAAAAGAGCTTTAAATATATATATACAGATGGCATGTTTACTTTATGTACTACATGCA	10304
QY	9417	CTTGCGTCGATAAAATGTGGTCAACAGCATTCGTCTTTGAAGGCGAGGTGCTTCAGGATACC	9476
Db	10305	CTTGCGTCGATAAAATGTGGTCAACAGCATTCGTCTTTGAAGGCGAGGTGCTTCAGGATACC	10364
QY	9477	ATATACAGCTCAGAAGTTTCTCTTTTAGGCATTAATAATTTTAGCAAGATATCTCATCTCT	9536
Db	10365	ATATACAGCTCAGAAGTTTCTCTTTTAGGCATTAATAATTTTAGCAAGATATCTCATCTCT	10424
QY	9537	TCCTTTTAAACCATTTTCTTTTTTCTGGTTAGAAAAGTTATGTCAGAAAAAGTAAATGCG	9596
Db	10425	TCCTTTTAAACCATTTTCTTTTTTCTGGTTAGAAAAGTTATGTCAGAAAAAGTAAATGCG	10484
QY	9597	ATTTACGCTCATGTGAGAAAAGCTATAAAATGAATACAAATTAAGAGCTGTTATTTAAATTAG	9656
Db	10485	ATTTACGCTCATGTGAGAAAAGCTATAAAATGAATACAAATTAAGAGCTGTTATTTAAATTAG	10544
QY	9657	CCAGTGA AAAA ACTATTAACAACCTGCTATTACCTGTTAGTATATTGTTGCGATTAAAAA	9716
Db	10545	CCAGTGA AAAA ACTATTAACAACCTGCTATTACCTGTTAGTATATTGTTGCGATTAAAAA	10604
QY	9717	TGCATATACTTTAAATAATGTATATTGTTATGCTATACGCAATTTATTTGAAGTTCCTT	9776
Db	10605	TGCATATACTTTAAATAATGTATATTGTTATGCTATACGCAATTTATTTGAAGTTCCTT	10664
QY	9777	GTTCACTGTGTATATACCTTAATCGCTTGTGCATTTTGGAGACATTTATTTTGCCTGCTA	9836
Db	10665	GTTCACTGTGTATATACCTTAATCGCTTGTGCATTTTGGAGACATTTATTTTGCCTGCTA	10724
QY	9837	ATTTCTTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCG	9896
Db	10725	ATTTCTTTTACATTTTGTCTTACGGAATATTTTCATTCAACTGTGGTAGCCGAATTAATCG	10784
QY	9897	TGTTTCTTCACTTAGGGACATGTGCGTCCTAAGTTGTAAAGACATTTGTTATTACCAAGC	9956
Db	10785	TGTTTCTTCACTTAGGGACATGTGCGTCCTAAGTTGTAAAGACATTTGTTATTACCAAGC	10844
QY	9957	AAACCATCTCTGAAAGCATATGACAAAATATTTCTCTCTTAATATCTTACTATACCTGAAAG	10016
Db	10845	AAACCATCTCTGAAAGCATATGACAAAATATTTCTCTCTTAATATCTTACTATACCTGAAAG	10904
QY	10017	CAGACTGCTATAAGCGTTCACTTACTCTTCACTCATPAAGGAAATGTTTACAATTAAT	10076
Db	10905	CAGACTGCTATAAGCGTTCACTTACTCTTCACTCATPAAGGAAATGTTTACAATTAAT	10964
QY	10077	TATTAGGTAAGCATTTGTTTTATATTGGTTTTATTTTCACTTGGCGTGAGATTTCAAGNAA	10136
Db	10965	TATTAGGTAAGCATTTGTTTTATATTGGTTTTATTTTCACTTGGCGTGAGATTTCAAGNAA	11024
QY	10137	CACCCAGCTCTCACAGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTG	10196
Db	11025	CACCCAGCTCTCACAGTAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTG	11084
QY	10197	GCCTGTTAAATTTTTTAAATAGAAATTTTAAGTCCTCATTTTCTTTCCGGTGTTTTTAAAGC	10256
Db	11085	GCCTGTTAAATTTTTTAAATAGAAATTTTAAGTCCTCATTTTCTTTCCGGTGTTTTTAAAGC	11144
QY	10257	TTAATTTTCTCGGCTTTATTCATAAAATCTTTAAGTCAACTACATTTTGAAAAATCAAGA	10316
Db	11145	TTAATTTTCTCGGCTTTATTCATAAAATCTTTAAGTCAACTACATTTTGAAAAATCAAGA	11204
QY	10317	CCTGCATTTTAAATTTCTTATTACCTCTGGCAAAACCATTTCAAAACCATGGTAGTAAG	10376
Db	11205	CCTGCATTTTAAATTTCTTATTACCTCTGGCAAAACCATTTCAAAACCATGGTAGTAAG	11264
QY	10377	AGAAAGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGAT	10436
Db	11265	AGAAAGGTGACACCTGGTGGCCATAGGTAAATGTACCACGGTGGTCCGGTGACCAGAGAT	11324
QY	10437	GCAGCGCTGAGGGTTTTTCTCTCAAGGTAAAGGAATTAAGAAATTTGGGTGGAGGGCGCTGCAC	10496

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Db 11325 GCAGCGCTGAGGGTTTCTCTGAAGGTAAAGGAATAAGGATGGGTGGAGGGCGTGCACCT 11384
QY 10497 GGAATACACTGTGAGAAAAGCCCTGAAAATTTGAGAAAAACAACAAGAACTACTTTA 10556
Db 11385 GGAATACACTGTGAGAAAAGCCCTGAAAATTTGAGAAAACAACAAGAACTACTTTA 11444
QY 10557 CCAGCTATTGAAATGCTGGAATTCACAGGCCCATTCGCTGAGCTGCCTGAACTGGGAACACA 10616
Db 11445 CCAGCTATTGAAATGCTGGAATTCACAGGCCCATTCGCTGAGCTGCCTGAACTGGGAACACA 11504
QY 10617 ACAGAGGAAAACAACCACTCTGTAATCAATTCAGTCAAGTACAGCAGGTGATTGAGGA 10676
Db 11505 ACAGAGGAAAACAACCACTCTGTAATCAATTCAGTCAAGTACAGCAGGTGATTGAGGA 11564
QY 10677 CTGCTGAGAGGTACAGGCCAAAATTCCTATGTTGTTATTAATAATGTCATCTTTATAATA 10736
Db 11565 CTGCTGAGAGGTACAGGCCAAAATTCCTATGTTGTTATTAATAATGTCATCTTTATAATA 11624
QY 10737 CTGCTAGATTTTATAAAACATTCCTCAAACTCACACACATTTAAAAACAAAACACTG 10796
Db 11625 CTGCTAGATTTTATAAAACATTCCTCAAACTCACACACATTTAAAAACAAAACACTG 11684
QY 10797 TCCTAAATCCCAATTTTTCATAAC 10825
Db 11685 TCCTAAATCCCAATTTTTCATAAC 11713

RESULT 13
AL359892/c
LOCUS
DEFINITION Homo sapiens chromosome 6 clone RP11-557F22, *** SEQUENCING IN
PROGRESS ***, 18 unordered pieces.
ACCESSION AL359892
VERSION AL359892.5 GI:9930971
KEYWORDS HTG: HTGS_PHASE1; HTGS_CANCELLED.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 193752)
AUTHORS Sims, S.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 27, 2000 this sequence version replaced gi:9864230.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA557F22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 183925 bases at least Q40
Consensus quality: 187703 bases at least Q30
Consensus quality: 189658 bases at least Q20
Insert size: 192052; sum-of-contigs
Insert size: 198247; agarose-fp
Quality coverage: 3.68x in Q20 bases; sum-of-contigs Quality
coverage: 3.70x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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* be preserved.
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: US-09-497-957-1

Perfect score: 10825
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10823	100.0	10825	22 AAC68425	Human hereditary h
2	10823	100.0	10825	22 AAC68426	Human hereditary h
3	10823	100.0	10825	22 AAC68427	Human hereditary h
4	10823	100.0	10825	22 AAC68428	Human hereditary h
5	10816.6	99.9	10825	18 AAT96690	Hereditary haemoch
6	10759.8	99.4	12146	21 AAA96794	Genomic DNA of a h
c	7	10707	98.9	237326	Hereditary haemoch
	8	5724.8	52.9	5749	Human musculoskele
c	9	3109	28.7	235033	Hereditary haemoch

c	10	2556.4	23.6	8622	24	ABL34142	Human immune syste
	11	2248.8	20.8	8622	24	ABL34143	Human immune syste
	12	1712	15.8	1712	22	AAAL36748	Human musculoskele
	13	1051.6	9.7	2506	21	AAA96769	CDNA sequence enco
	14	1051.6	9.7	2727	19	AAV23523	Haemochromatosis g
	15	516	4.8	517	22	AAC68440	Human hereditary h
	16	516	4.8	517	22	AAC68441	Human hereditary h
	17	439	4.0	1110	22	AAAL36752	Human musculoskele
c	18	395.2	3.7	12127	22	ABA08204	Human ovarian and
c	19	395.2	3.7	12127	22	AAAL07512	Human reproductive
c	20	395.2	3.7	12127	22	AAAL28679	Genomic sequence #
	21	384	3.5	384	22	AAAL36751	Human musculoskele
	22	358	3.3	359	20	AAAL60055	Hereditary hemochr
	23	357.6	3.3	161425	22	AAH02340	Human AKAP10 gene
	24	357.6	3.3	162025	22	AAH02339	Human AKAP10 gene
	25	355.8	3.3	14796	19	AAV27941	Survivin gene. Ho
	26	355.8	3.3	14796	22	AAAL1523	DNA encoding human
	27	355.8	3.3	14796	22	AAH47531	Human Her-3 genomi
	28	355	3.3	48045	22	AAK84730	Human immune/haema
	29	355	3.3	48045	22	AAK85984	Human immune/haema
	30	351.2	3.2	32190	22	AAAS6709	Human cardiovascular
	31	347.8	3.2	48037	22	AAK84729	Human immune/haema
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	35	338.6	3.1	14781	22	AAAL36303	Human musculoskele
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	37	337.6	3.1	31885	22	AAAL36165	Human musculoskele
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	39	337.6	3.1	31885	22	AAAL04523	Human reproductive
c	40	337.6	3.1	31885	22	AAAS28341	Genomic sequence #
	41	337.6	3.1	52845	22	AAK71437	Human immune/haema
c	42	337.2	3.1	32763	22	AAK68779	Human immune/haema
c	43	336.6	3.1	32187	22	AAAS32249	Human DNA repair a
c	44	336.4	3.1	12473	22	ABA18817	Human nervous syst
c	45	334.2	3.1	53552	22	AAAS13655	Genomic DNA sequen

ALIGNMENTS

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RESULT 1
AAC68425
ID AAC68425 standard; DNA; 10825 BP.
XX AAC68425;
AC
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX
XX US6140305-A.
XX
PD 31-OCT-2000.
XX
XX 04-APR-1997; 97US-0834497.
XX
XX 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
XX (BIRA ) BIO-RAD LAB INC.
XX
XX Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
XX Feder JN;
XX WPI: 2001-006341/01.
XX P-PSDB; AAB36869.

```

XX New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
XX Sequence 10825 BP; 2998 A; 2253 C; 2648 G; 2926 T; 0 other;
SQ

Query Match 100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
AAC68426
ID AAC68426 standard; DNA; 10825 BP.
XX
AC AAC68426;
XX
DT 21-FEB-2001 (first entry)
XX
DE Human hereditary hemochromatosis 24d1 mutation DNA.
XX
KW HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ds.
XX
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PE 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
DR WPI: 2001-006341/01.
DR P-PSDB; AAB36870.

XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload.
XX
PS Disclosure; Fig 3; 108pp; English.
XX
CC The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2999 A; 2253 C; 2647 G; 2926 T; 0 other;

Query Match 100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 1 tctaaagttgagataaaatttttaaatgtatgattgaattttgaaatcataaataatta 60

QY 61 AATATCTAAAGTTTCAGATCAGAACATTGCGAAGCTACTTTCCCAATCAACACACCCCT 120
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QY 1141 CTAGGCTTTATTGATTGCAATGTCTGTAAATTAAGAGGCGCTCTCTACAAAGTACTGA 1200

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Db	3901	tccatgggtttccagtagaatttcaagccagatgtggcgtgcagctggagtcagagtcgtaa	3960
Qy	3961	AGGTTGGGATCACATGTTCACTGTGTGACTTCTFGSACTATTATGAAAATCACAAACACAG	4020
Db	3961	agggtgggatcacatgttcaactgttgactctcgtgactattatggaaaatcacaaccacag	4020
Qy	4021	CAAGGTTATGTGAGAGGGGGCCTCACCTTCTGAGGTGTGCAGAGCTTTTCATCTTTTC	4080
Db	4021	caaagggtatgtggagagggggcctcacctcctgaggtgtgcagagcttttcactctttc	4080
Qy	4081	ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAAGAGGGAAG	4140
Db	4081	atgcattctgaagaaacagctggaagtctgaggtctctgtggggagcagggaaggggaag	4140
Qy	4141	GAAITTTGCTTCTFGAGATCATTTTGTGTCTCTGGGATGGTGGAAATAGGGACCTATTTCCTT	4200
Db	4141	gaatttgcttccctgagatcatctgtgctcttgggatgggtgaaatagggccatttccctt	4200
Qy	4201	TGTTTGCAGTTAACRAGGCTGGGGATTTTTCCAGNGTCCACACCCCTGCAGGTATCTCTG	4260
Db	4201	tgttctcagttaaccaaggtctggggattttccagagttcccaacccttcgaggttcactctg	4260
Qy	4261	GGCTGTGAATGCACAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	ggctgtgaaatgcaagaagacaacagtacccgagggctactggaaatcacgggtatgatggg	4320
Qy	4321	CAGACCACTTGAATPCTGCCCCTGACACACTGTGATTGGAGCAGACAGAACCCAGGGCC	4380
Db	4321	caggacacacttgaa ttctgcctgacacactggatiggagagcagcagaacccaagggcc	4380
Qy	4381	TGGCCCCCAAGCTGGAGTGGGAAGGCACAGAATTTCGGGCCAGGCAGACAGGGCTTAC	4440
Db	4381	tggcccccaagctggagtgggaaggcacaagattcgggccaggcagacaagggcctac	4440

QY	4441	CTGGAGAGGGNACTGCCCTGTCACACAGCTGCAGCAGTTCCTGGAGCTGGGAGAGGTGTTTGTG	4500
Db	4441	ctggagagggactgcgcctgcacagctgcagagctgcagagtgctgcgagctggggagaggtgttttg	4500
QY	4501	GACCAACAAGGTATGTGTGGAAACACACACTTCTGCCCCATATACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	gaccaacaaggtatgtgtggaacacacactctgcacctatactctagtgcagagctggaggg	4560
QY	4561	AGTTTGACGGGCACGGNAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	aggttgcagggcacggaaatccctggctgggtggagtttcagaggtggctgaggtgtgtgcctc	4620
QY	4621	TCCAAATCTCTGGGAAGGCACTTTCTCAATCCCTAGAGTCTCTACCTTATAAATTTGAGAGCTA	4680
Db	4621	tcceaaatctctgggaagggactttctccaaatccctcagagctctcacctatacaattgagagtga	4680
QY	4681	TGAGACAGCCACAAAGTCATGGGTTTAAATTTCTTCTCCATGCATATGGCTCAAAAGGAA	4740
Db	4681	tgagacagccacaaagtcattgggttaattttcttcacatgcatatggctcaaaaggaa	4740
QY	4741	GTGTCATGCCCCCTGCTTTTATTTTAAACCAATATCTTTTGTATATTTATACCTGTATAA	4800
Db	4741	gtgctatggcccttgctttttatttaaaccataatcttttgtattattatcacctgttaa	4800
QY	4801	AAATTCAGAAATGCTCAAGGCCGGCAGCGTGCTCACCCCTGTAATCCACGACACTTTGGG	4860
Db	4801	aaattcagaatgtcaagccgggcacggtggtccacccctgtaatcccaagcactttggg	4860
QY	4861	AGGCCGAGGCGGTGGTCACAGGTCAGAGTTTGAGACACGCGTGCACCAACATPGTGAA	4920
Db	4861	agggcaggcggtgggtcacaaggttcagagtttgagaccagcctgaccaacaatggtaa	4920
QY	4921	ACCCGTCCTTAAAAAATAACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA	4980
Db	4921	accgctctcaaaaaatacaaaaattagctgggtccaaagtcacgtgcacctgtagtccca	4980
QY	4981	GCTAATTTGAAGCCTGAGCGAGAGCATCGCTTGTAACCTGGGAAGCGGAAGTTGCACTGA	5040
Db	4981	gctaattggaagcgtgagcgaggagcatcgcttgaaacctgggaagcggaagtgtcactga	5040
QY	5041	GCCAAGATCGCGCACTGCACACTCCAGCTTAGCGACGACAGTGAGACTCCATCTTAAAAA	5100
Db	5041	gccaaagtgcgcacctgcactccagcctcaggcagcagtgagactccatctcaaaaa	5100
QY	5101	AAAAAATAAAAAAAGAAATTCAGAGATCTCAGCTATCATATGAATACCAAGACAAA	5160
Db	5101	aaaaaataaaaaaagaaattcagagatctcagagatcctcagctcatcatgaataccaggacaa	5160
QY	5161	ATATCAAGTCAGCGCCACTTATCAGAGTAGAAGATCCCTTTAGGTAAAGTTTCTTTCAT	5220
Db	5161	atatcaagtgcggccacttatcagagtgaagaatcccttaggttaaaagtcttcttcat	5220
QY	5221	AGAACATAGCAATTAATCACTGAAGCTACTCTTTACAAGTCCGCTTCTTTATAACAATGC	5280
Db	5221	agaacatagcaataaatacactgaagctacctatcttaagtcgcgtctctataacaatgc	5280
QY	5281	CTCCTAGGTTGACCGAGGTGAACCTGACATCTGTATTCAATCAATTTTCAATGCACATAA	5340
Db	5281	ctcctaggttgacccaggtgaacctgaacctgtgtattcaatcatcttcaatgacataa	5340
QY	5341	AGGGCAATTTTATCTATCAGAAACAAGAACATGGGTAAACAGATATGATATTACATGTG	5400
Db	5341	agggcaattttatctatcagaaacaagaacatgggttaacagatagtcataattcacatgtg	5400
QY	5401	AGGAGAACAGCTGATCTGACTGCTCTCCAAGTGCACATGCTGTTTAGAGTCCCAATCTTAGG	5460
Db	5401	aggagacaagctgactgactgctctccaagtgacactgtgttagagtcaccaatcttagg	5460
QY	5461	ACACAAAATGGTCTCTCCTCTAGCTTGTGTTTTTCTGAAAAAGGTATTTCCTTCTCTCC	5520
Db	5461	acacaaaaatgggtctctcctctagcttgtttttctgaaaaaggtatttctctctctcc	5520
QY	5521	AACTATAGAAGGAGTGAAGGTTCCAGTCTCTCTGCGCAAGGGTAAACAGATCCCTCTC	5580

Qy	7741	GCACCTGTCCAGAAAAAGCATCATGCTATCTGTGGGTAGTAGATGGGTGTTTTTAGC	7800
Db	7741	gcacctgtcccagaaaaagcatcatgctatctgtgggtagtagatgggtgttttttagc	7800
Qy	7801	AGSTAGAGGCAAAATATCTTGAAGGGGTGTGAAGAGGTGTTTTTCTAAATGGCATGA	7860
Db	7801	aggcaggaggcaaatatcttgaaggggtgtgaaaggggtgttttttcttaatttggcatga	7860
Qy	7861	AGGTGTCATACAGATTTGCCAAGTTTAATGTCGCCCTTCATTTGGGATGCTACTAGTAT	7920
Db	7861	agggtgcatacagatttgcaaaagttaattggtgccttcatttgggtgctactctagtat	7920
Qy	7921	TCCAGACCTGAAGAATCACATAATTTTCTACCTGGTCTCTCTGTCGTGCTGATAAATGAAA	7980
Db	7921	tccagacctgaagaatcacataatttctacctggctctctctgttctcgataaagaaa	7980
Qy	7981	ATTATGATAAGGATGATAAAGCACTTACTTCTGTGTCGGACTCTCTCTGAGCAGCTACTTA	8040
Db	7981	attatgataaggatgataaagcaacttacttctgtgtccgactcttctgagcactactta	8040
Qy	8041	CATGATTACTGTCATGTCATCTTCTACAAATATTTCTATGAGATAGGTACTATTTATCCCAT	8100
Db	8041	catgattactgcatgcatctcttacaataattctatgagataggtactattatcccat	8100
Qy	8101	TTCTTTTTTAATGAAGAAAGTGAAGTAGGCCGGGACGGTGGCTCACGCCCTGTAATCCC	8160
Db	8101	ttcttttttaaatgaagaaagtgaagtaggccgggacgggtggctcacgccctgtaatccc	8160
Qy	8161	AGCACTTTGGGAGGCCAAAGCGGTGGATCACAGGTCAGGAGATCAGACCACTTCCTGGC	8220
Db	8161	agcactttgggagggccaaagcggtggatcacgaggtcaggagatcgagaccatccctggc	8220
Qy	8221	TAACTGTGTAAACCCCATCTCTAATAAATACAAAATTAAGCTGGCGTGTGGCAG	8280
Db	8221	taactgtgtaaaccccatctctataaaaaatacaaaaaattagctgggggtggcgag	8280
Qy	8281	ACGCCGTGTAGTCCAGCTACTCGGAAGGCTGAGGACAGAGAAATGGCATGAACCCAGGAGG	8340
Db	8281	acgccgtgtagtccagctactcgaaggtgagcgagagaatggcatgaacccaggagg	8340
Qy	8341	CAGAGCTTGCGAGTAGCGAGTGTGGCCACTGCACTCCAGCCCTAGGTGACAGAGTGAGA	8400
Db	8341	cagagcttgagtagcgaggtttgcccactgcactccagccctaggtagacagagtgaga	8400
Qy	8401	CTCCATCTCAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	8460
Db	8401	ctccatctcaaaaaataaaaaataaaaaataaaaaataaaaaataaaaaataaaaaata	8460
Qy	8461	TAGAGTATCTCATAGTTTGTGATAGAAACAGGTTTCAAACTCAGTCAATCTGACCG	8520
Db	8461	tagagtatctcatagtttgtcagtgatagaaacaggtttcaaaactcagtcactctgaccg	8520
Qy	8521	TTTGATACATCTACACACCCTACTATTCAGTAGTTTAGATGCCCTAGATAAANTAGAAA	8580
Db	8521	tttgatacatctcacaccactactatccagtagtttagatgcctagataaataagaaa	8580
Qy	8581	GGAAGGAGATGGCTCTCTCTGTCATTTGTTTCTCTGAGTGAGCTTGAATTCACAT	8640
Db	8581	ggaaaggagatggctctctctgctcatttggtttctctgagtgagcttgagctggaatcacat	8640
Qy	8641	GAAGGGAAACACAGAAAAACCAACCTGATCCTCAGCTGTCATGCTTTTCTTTAAAGTC	8700
Db	8641	gaagggaaacacagaaaaacccaacagatcctcagctgctcatgttttcccttaaaagtc	8700
Qy	8701	CCTGAGGAAGCTCCTGGAATCTGACTCCCTTGCTCTCTGTCCTCTCTGTCCTTTGGCATTCA	8760
Db	8701	cctgaaggaggtccttggaatctgactcccttgctctctgctctctgtgtctcttttggcatca	8760
Qy	8761	TTTCTTTGGACCTACGCAAGGACGTAAATTTGGTGGGACAGCTAGTGGCCCTGCTGGGC	8820
Db	8761	tttctttggacctacgcaaggactgtaatttgggggacagctagtgccctgctgggc	8820
Qy	8821	TTTCACACGGGTGCTCCTCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTC	8880
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Qy	8881	CCTCAATGAAGTGGAGTAGCTCTCTCATTTTGTAGATGGTATATAATGAAGCCACCAAGTG	8940
Db	8881	cctcaatgaagtggagtagactctctcattttgagatggataataatgggaagccaccaagt	8940
Qy	8941	GCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCGGTCCGACACATTAATAAAA	9000
Db	8941	gcttagagatgccaggctccttccatggagccactg999tcccg9tgcacattaaaaa	9000
Qy	9001	AAAAATCAACAGGACATTCAGGAATTTGTAGATTTGGGAAATCAGTTCACCATGTTC	9060
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Qy	9061	AAAGAGTCTTTTTTTTTTTTTTTTGACACTATTTGCCAGGCTGGAGTGCAATGGCATGAT	9120
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Qy	9121	CTCGGCTCACTGTAACTCTGCTCCAGGTTCAAGCGATTTCTCTGTCTCAGCCTGCCA	9180
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Qy	9181	AGTAGCTGGGATTTACAGGCGTGACACCATGCCCGCTAAATTTTGTATTTTGTAGTAGA	9240
Db	9181	agtagctgggatttacaggcggtgcaccacatgcccggctaattttgtatttttagtaga	9240
Qy	9241	GACAGGTTTCACCATTTTGGCCAGGCTGCTCGAACCTCTCCTGACCTCGTATCCGCC	9300
Db	9241	gacaggtttccacatagttggccagggtgtctcgaaactctcctcgacctcg1gatccgcc	9300
Qy	9301	TGCGCTCGGCTCCCAAGTGTGAGATTACAGGTGTGAGCCACCCCTGCCAGCCGCTCAAA	9360
Db	9301	tgctcgctcgctcccaaggtgtgagattacagggtgagccaccctgcccagcgctcaaa	9360
Qy	9361	AGAGTCTTAAT	9420
Db	9361	agagcttaataataataataataataataataataataataataataataataataataata	9420
Qy	9421	GCTGCATAAATGTGTACAAAGCATTTCTTGAAGGCGAGGTGCTTCAGAGTACCATAT	9480
Db	9421	gctgcataaaatgtgttgaagcattctctgtcttgaagggcaggtgcttcaggataccatat	9480
Qy	9481	ACAGCTCAGAAAGTTCCTTTTAGGCATTAATTTTAGCAAGATATCTCATCTCTCTT	9540
Db	9481	acagctcagaagttctcttcttttaggcattaaatttttagcaagatactctcatctctct	9540
Qy	9541	TTAAACCATTTTCTTTTGTGTTAGAAAGTGTATAGTAAAGTAAATGTGATTT	9600
Db	9541	ttaaacattttcttttttgggttagaaaagttatgtagaaaaagtaaa1gtagttt	9600
Qy	9601	ACGCTATTGTAGAAAAGCTATAAAATGAATACAATTAAGCTGTTATTTAAATAGCCAG	9660
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Qy	9661	TGAAAACTATTAAACAACCTGCTATTACCTGTTAGTATTATTTGTTCCATTAATAATGCA	9720
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Db 10681 tgaaggtacagggccaaaactcttaagtgtgtaataaataatgctatcttaataactgt 10740
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QY 10801 TAAAAATCCCAATTTTTCATAAAC 10825
Db 10801 taaaatcccaaatttttcataaac 10825

RESULT 3
AAC68427
ID AAC68427 standard; DNA; 10825 BP.
XX
AC AAC68427;
XX
DT 21-FEB-2001 (first entry)
XX
DE. Human, hereditary hemochromatosis 24d2 mutation DNA.

XX
KW HH; hereditary hemochromatosis; chelation agent;
XX T-cell differentiation factor; iron overload; ds.
OS Homo sapiens.
XX
PN US6140305-A.
XX
PD 31-OCT-2000.
XX
PF 04-APR-1997; 97US-0834497.
XX
PR 04-APR-1996; 96US-0630912.
PR 16-APR-1996; 96US-0632673.
PR 23-MAY-1996; 96US-0652265.
XX
PA (BIRA) BIO-RAD LAB INC.
XX
PI Thomas WJ, Drayna DF, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
XX WPI; 2001-006341/01.
DR P-PSDB; AAB36871.
XX
XX New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -
XX
XX Disclosure; Fig 3; 108pp; English.
XX
XX The present invention relates to hereditary hemochromatosis gene
CC products. These proteins may be used to treat a patient diagnosed as
CC having human hemochromatosis disease. It is also useful as a metal
CC chelation agent or as a T-cell differentiation factor, and for
CC alleviating iron overload. They may also be used in protein replacement
CC therapy for individuals having a defective human hemochromatosis gene.
XX
SQ Sequence 10825 BP; 2998 A; 2252 C; 2649 G; 2926 T; 0 other;

Query Match 100.0%; Score 10823; DB 22; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TCTAGGTTGAGATAAATTTTAAATGTATGATTGAAATTTGAAATTCATAAATATTTA 60
Db 1 tctaaggttgagataaaatttttaaatgtatgattgaattttgaaaatcataaattatta 60
QY 61 AATATCTAAGTTCAGATCAGAACATTTCGAGGCTACTTCCCAANTCAACAACACCCT 120
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QY 121 TCAGGATTTAAAAACAAAGGGGACACTGGATTCAGCTAGTGTTCACAGCAGGTACTCT 180
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QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCGTAAGACCTGTTGCTTTACACAGGAAGTT 240
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Db 361 atggcccgcgagccagcgccgctctctctctctctctctctctctctctctctctctg 420
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XX 05-OCT-2000.

XX 24-MAR-2000; 2000WO-US07982.

XX 26-MAR-1999; 99US-0277457.

XX (BILL-) BILLUPS-ROTHENBERG INC.

XX Rothenberg BE, Sawada-Hirai R, Barton JC;

XX WPI; 2000-647244/62.

XX Diagnosing an iron disorder e.g. hemochromatosis or a genetic
 PT susceptibility to develop it, by determining the presence of a mutation
 PT in exon 2 or an intron of a histocompatibility iron loading nucleic
 PT acid -

XX Example 1; Page 21-28; 55pp; English.

XX The present sequence represents the human histocompatibility iron
 CC loading (HFE) gene. The HFE gene is a major histocompatibility (MHC)
 CC non-classical class I gene located on chromosome 6p. Mutations in the
 CC gene lead to iron disorders. The specification describes a method for
 CC diagnosing an iron disorder or a genetic susceptibility to develop the
 CC disorder in a mammal. The method comprises determining the presence of
 CC a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
 CC is not a C to G missense mutation at nucleotide 187 of the sequence
 CC given in A96769 (Genbank Accession number U60319). The presence of the
 CC mutation indicates the disorder or the genetic susceptibility to the
 CC disorder. The method is used to diagnose an iron disorder
 CC e.g. haemochromatosis, or a genetic susceptibility to develop it.

XX Sequence 12146 BP; 3383 A; 2474 C; 2911 G; 3378 T; 0 other;

Query Match 99.4%; Score 10759.8; DB 21; Length 12146;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 10812; Conservative 0; Mismatches 9; Indels 8; Gaps 4;

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 Db |
 1429 tcaacccaatccgcaagccctctccctactttctgcgtccagagaccgcgtgagggagtgc 1488
 QY 601 CTACCACTGAACCTCAGATAGGGTCTCTCGCCCCCAGACCTGCCCCCTCCCCCGGCTGT 660
 Db |
 1489 ctaccactgaactcagataggggtccctcgccccaggaactgcgccctcccccggtgt 1548
 QY 661 CCCGGCTCTCGGAGTGAATTTTGGAAACCGCCACTCTTCCCTCCCACTAGATGCTTT 720
 Db |
 1549 cccggctctcgggagtgaactttggaaaccccaactcccttcccccaactagatgcttt 1608
 QY 721 TAAATAAATCTCGTAGTTCCTCACTTGAGCTGAGCTAAGCCTGGGGCTCCTTTGAACCTGG 780
 Db |
 1609 taataaaatctcgtagttcctcacttgagctgagctgaagcctggggtccttgaacctgg 1668
 QY 781 AACTCGGGTTTATTTCCAAATGTACGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 840
 Db |
 1669 aactcgggtttatttccaatgtagctgtgcagtttttccccagtcacttcccaacagg 1728
 QY 841 AAGTTCTTCCTCGTAGTCTTCCCGAGAAAGGCTGAGCAAAACCCACAGCAGGATCGCACGG 900
 Db |
 1729 aagttcttccccctgagttcgttgcgcagagaagcgtgagcaaacccacagcagatccgcacgg 1788
 QY 901 GGTTCACCTCAGAACGAATGCTTGGGGGTGGGGCGCGAAGAGTGGCGTGGGGA 960
 Db |
 1789 ggtttccacctcagaacgaatgcgttggcggttggggcgcgaaagagtggtgtggga 1848
 QY 961 TCTGAATCTTCACCATTCACCCACTTTTGGTGAGACCTGGGGGTGAGGCTCTCTAGGGT 1020
 Db |
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 QY 1021 GGGAGGCTCTGAGAGAGGCTTACTCGGCTTTTCCCACTTCTTGCATTTGTCCTTTT 1080
 Db |
 1909 gggaggctcctgagagagggcctacctcggccttccccactcttggcaattgtctttt 1968
 QY 1081 GCCTGGAAATTAAGTATATGTTAGTGTGAAACGTTTGAACGTTTGAACGTTTGAACGTTT 1140

[illegible]

Db	44762	ACAGTGATCTGTCACAGCGCTTTTAAAGATTGCTCTGGCTATGTGGAAAGCAGAATG	44700
Qy	2401	AAGGGAGCAACAGTAAAGCAGGAGGCCAGCCAGGAAAGCTGTTACACAGTCCAGGCAAG	2460
Db	44702	AAGGAGCAACAGTAAAGCAGGAGGCCAGCCAGGAAAGCTGTTACACAGTCCAGGCAAG	44643
Qy	2461	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAGGGAGTGACAAACCATTTGTCTCCTGAA	2520
Db	44642	AGGTAGTGGAGTGGGCTGGGTGGGAACAGAAAGGGAGTGACAAACCATTTGTCTCCTGAA	44583
Qy	2521	TATATTCTCAAGGAAGTTGCTGAAGGATTTCTATGTTCTGTGAGAGAAAGAGAATTTGG	2580
Db	44582	TATATTCTCAAGGAAGTTGCTGAAGGATTTCTATGTTCTGTGAGAGAAAGAGAATTTGG	44523
Qy	2581	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGACAGATTTCTTGAGCTCAGGA	2640
Db	44522	CTGGGTGTAGTAGCTCATGCCAAGGAGGAGGCCAAGGAGACAGATTTCTTGAGCTCAGGA	44463
Qy	2641	GTTCAAGACCGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	2700
Db	44462	GTTCAAGACCGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA	44403
Qy	2701	GCTTGGGTGTGGTGGCATGCACCTGTGTATCTTAGCTACTCGGAGGCTGAGGTGGAGGTA	2760
Db	44402	GCTTGGGTGTGGTGGCATGCACCTGTGTATCTTAGCTACTCGGAGGCTGAGGTGGAGGTA	44343
Qy	2761	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	2820
Db	44342	TTGCTTTGAGCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC	44283
Qy	2821	CTAGGTGCAGAGCAAGACCCCTGTCTCCCTTGACCCCTGAAAGAGAGAGATTAAAGT	2880
Db	44282	CTAGGTGCAGAGCAAGACCCCTGTCTCCCTTGACCCCTGAAAGAGAGAGATTAAAGT	44223
Qy	2881	TGACTTTTGTCTTTATTTTAAATTTATTTGSCCTGAGCAGTGGGGTAATTTGGCAATGCCAT	2940
Db	44222	TGACTTTTGTCTTTATTTTAAATTTATTTGSCCTGAGCAGTGGGGTAATTTGGCAATGCCAT	44163
Qy	2941	TTCTGAGATGGTGAAGGCGAGAGAAAGCAGATTGGGGTAAATCAAGGATCTGCATTTTG	3000
Db	44162	TTCTGAGATGGTGAAGGCGAGAGAAAGCAGATTGGGGTAAATCAAGGATCTGCATTTTG	44102
Qy	3001	GGACATGTTAAGTTTGAGATTCCAGTCCAGGTTTCCAAAGTGGTGAGGCCACATAGGCAATT	3060
Db	44103	GGACATGTTAAGTTTGAGATTCCAGTCCAGGTTTCCAAAGTGGTGAGGCCACATAGGCAATT	44044
Qy	3061	CAGTGTAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCAGCACT	3120
Db	44043	CAGTGTAAGAAATTCAGGACCAAGGCTGGGCACGGTGGCTCACTTCTGTAATCCAGCACT	43984
Qy	3121	TTGGTGGCTTGAGGCAGGTAGATCATTTTGAGTCAAGGATTGAGACAAGCTTTGGCCACA	3180
Db	43983	TTGGTGGCTTGAGGCAGGTAGATCATTTTGAGTCAAGGATTGAGACAAGCTTTGGCCACA	43924
Qy	3181	TGTTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCCACGCCT	3240
Db	43923	TGTTGAAACCCCATGTCTACTAAAAATACAAAAATTAGCCTGGTGTGGTGGCCACGCCT	43864
Qy	3241	ATAGTCCCAGGTTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	3300
Db	43863	ATAGTCCCAGGTTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGGTGCAGG	43804
Qy	3301	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGGAGACTCTGT	3360
Db	43803	TTGCAGTGAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGGAGACTCTGT	43744
Qy	3361	CTC----AAATTTTCTTCAGGATT	3416
Db	43743	CTCAATTTTCTTCAGGATT	43684
Qy	3417	TGGGTCTAATTTTGCCCTGAGACACCACTCTGTAGTTCAACTACCATTCAGCTAGACACACT	3476
Db	43683	TGGGTCTAATTTTGCCCTGAGACACCACTCTGTAGTTCAACTACCATTCAGCTAGACACACT	43624

QY	4557	GAGGAGGTGTCAGGGCACGGAAATCCCTGGTGTGGAGTTTCAGAGGTGGCTCAGGCTGTGTG	4616
Db	42543	GAGGAGGTGTCAGGGCACGGAAATCCCTGGTGTGGAGTTTCAGAGGTGGCTCAGGCTGTGTG	42484
	QY	4617	CCTCTCAAATTCGCGAAGGGACTTTCAAATCCCTAGAGTCTCTACCTTATATATGAGA
Db	42483	CCTCTCAAATTCGCGAAGGGACTTTCAAATCCCTAGAGTCTCTACCTTATATATGAGA	42424
QY	4677	TGTATGAGACAGCCACAAGTCATGGGTAAATTTCTTTTCTCCATGTCATATGGCTCAAG	4736
Db	42423	TGTATGAGACAGCCACAAGTCATGGGTAAATTTCTTTTCTCCATGTCATATGGCTCAAG	42364
QY	4737	GGAAAGTGTCTATGGCCCTTGCTTTTATTAACCAATAATCTTTTGTATATTTATACCTG	4796
Db	42363	GGAAAGTGTCTATGGCCCTTGCTTTTATTAACCAATAATCTTTTGTATATTTATACCTG	42304
QY	4797	TTAAAAATTCAGAAATGTCAAGGCGGGCAGGTGGCTCACCCTGTAAATCCGAGCACTT	4856
Db	42303	TTAAAAATTCAGAAATGTCAAGGCGGGCAGGTGGCTCACCCTGTAAATCCGAGCACTT	42244
QY	4857	TGGGAGGCGGAGGCGGTGTGTCAAAGTCAAGAGTTTGAGACCAGGCTGACCAACATGG	4916
Db	42243	TGGGAGGCGGAGGCGGTGTGTCAAAGTCAAGAGTTTGAGACCAGGCTGACCAACATGG	42184
QY	4917	TGAACCCGCTCTCTAAAAAAATACAAAAATTTAGCTGTGTCACAGTCATGCGGACCTGTAGT	4976
Db	42183	TGAACCCGCTCTCTAAAAAAATACAAAAATTTAGCTGTGTCACAGTCATGCGGACCTGTAGT	42124
QY	4977	CCCAGCTAAATTTGGAGGCTGAGGAGGAGCATCGCTGAACCTGGGAAGCGGAAGTTGCA	5036
Db	42123	CCCAGCTAAATTTGGAGGCTGAGGAGGAGCATCGCTGAACCTGGGAAGCGGAAGTTGCA	42064
QY	5037	CTGAGCCAAGATCGCGCCACTGCATCCAGGCTTAGGCAGCAGAGTGAGACTTCCATCTTAA	5096
Db	42063	CTGAGCCAAGATCGCGCCACTGCATCCAGGCTTAGGCAGCAGAGTGAGACTTCCATCTTAA	42004
QY	5097	AAAAAATAATGAGAAATTCAGAGATCTCAGGTATCATATGAATACCCAGGA	5156
Db	42005	AAAAAATAATGAGAAATTCAGAGATCTCAGGTATCATATGAATACCCAGGA	41946
QY	5157	CAAAATATCAAGTGTAGGCGCACTTATCAGAGTAGAAGAAATCCTTTTAGGTTTAAAGTTTCTT	5216
Db	41945	CAAAATATCAAGTGTAGGCGCACTTATCAGAGTAGAAGAAATCCTTTTAGGTTTAAAGTTTCTT	41886
QY	5217	TCATAGAACATAGCAATATCACTCAAGCTACTCTTACAAGTCCGCTTCTTTATAACA	5276
Db	41885	TCATAGAACATAGCAATATCACTCAAGCTACTCTTACAAGTCCGCTTCTTTATAACA	41826
QY	5277	ATGCCTCTCTAGTTGACCCAGGTGAAACTGACCATCTGTATTCATCATTTTTCAATGCAAC	5336
Db	41825	ATGCCTCTCTAGTTGACCCAGGTGAAACTGACCATCTGTATTCATCATTTTTCAATGCAAC	41766
QY	5337	ATAAAGGCAATTTTATCTATCAGAACAAAGAACATGGTACACATATGTATATTTACA	5396
Db	41765	ATAAAGGCAATTTTATCTATCAGAACAAAGAACATGGTACACATATGTATATTTACA	41706
QY	5397	TGTGAGGACAACAAGCTGATCTGACTGTCTCCAAAGTCACACTGTGTGTAGAGTCCAATCT	5456
Db	41705	TGTGAGGACAACAAGCTGATCTGACTGTCTCCAAAGTCACACTGTGTGTAGAGTCCAATCT	41646
QY	5457	TAGGACACAAAATGGTGTCTCTCTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5516
Db	41645	TAGGACACAAAATGGTGTCTCTCTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	41586
QY	5517	CTCCACCTTATAGAAGGAAGTGAAGTTCAGTCTCTCTGGCAAGGTTAAACAGATCCCC	5576
Db	41585	CTCCACCTTATAGAAGGAAGTGAAGTTCAGTCTCTCTGGCAAGGTTAAACAGATCCCC	41526
QY	5577	TCFCTCATCTTCCCTCTTCTGTCAAGTGTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	5636
Db	41525	TCFCTCATCTTCCCTCTTCTGTCAAGTGTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	41466
QY	5637	GACCTCTTCAAGTGAACACATCTACGGTGTGGGCGCTTGAACCTACTACCCCAACATCAC	5696

Db 40385 GCTTAGCTATCACTACCAAAATTATGCATTTCTACCCCTGAACATTTGGTGTAGGAA 40326
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Db 40325 AAGAGAAATCAGAAAGCCAGCTCATACAGAGTCCAAGGTCCTTTGGGAATAATGGGTT 40266
QY 6837 ATGATCACTGGGGTGTCAATTGAAGGATCCTAAGAAAGGAGGACCAACGATCTCCCTTATAT 6896
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Db 39965 AACGTGAGTACACGACGCTGCAGACTCACTGTGGAAAGGAGACAAACTAGAGACTCA 39906
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Db 39845 AATTGCCCTGACGAACCTCCTTGATTTTAGCCCTTCCTGTTTCATTTCCCAAAAAGATTCC 39786
QY 7317 CCATTTAGTTTCTGAGTTCCTGCATGCGGGTATCCCTAGCTGTGACCTCTCCCTGGA 7376
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QY 7377 ACTGCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCCCTCCGTCACCTC 7436
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Db 39665 AGACACATACACCTATGTCAATTTCAATTTCCCTAATTTTGGAAAGGAGTCTCCTAAATTTGG 39606
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Db 39305 TAGCAGTGTAGGAGCAAAATATCTTGAAGGGTGTGTAAGAGTGTGTTTCTAATTGGC 39246

QY 7857 ATGAAGGTGTCATACAGATTTGCAAAAGTTTAATGTGGTCCCTTCATTTGGGATGCTACTCTA 7916
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QY 7917 GTATTTCCAGACCTTGAAGAATCACAATAATTTCTACCTGGTCTCTCTTGTCTCTGATAAT 7976
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QY 7977 GAAAAATTATGATTAAGGATGATAAAAACACTTACTTCTGTCCGACTCTTCTTGAGCACCTA 8036
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Db 38405 AGTCCCTGAAGGAGGTCTCGGAATGTGACTCCCTTGTCTCTGTTGCTCTCTTTGGCA 38346
QY 8757 TTCAATTTCTTTGGACCCCTACGCAAGGACTGTAATTTGGTGGGAGACGTAGTGGCCCTGCT 8816
Db 38345 TTCAATTTCTTTGGACCCCTACGCAAGGACTGTAATTTGGTGGGAGACGTAGTGGCCCTGCT 38286
QY 8817 GGGCTTTCACACGCTGTCTCCCTTAGGCCAGTGGCTCTGGAGTCAGAACTCTGTTGGTA 8876
Db 38285 GGGCTTTCACACGCTGTCTCCCTTAGGCCAGTGGCTCTGGAGTCAGAACTCTGTTGGTA 38226
QY 8877 TTTCCCTCAATGAAGTGTGAGTAAAGCTCTCTCATTTTGAGATGGTATATGGAAGCCACCA 8936
Db 38225 TTTCCCTCAATGAAGTGTGAGTAAAGCTCTCTCATTTTGAGATGGTATATGGAAGCCACCA 38166

XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-451937/48.
 XX Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the musculoskeletal system including
 PT musculoskeletal cancers and also for testing and detection e.g.
 PT diagnosis -
 XX
 PS Example 2; SEQ ID NO 3112; 781pp + Sequence Listing; English.
 XX
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
 CC (AB03087-AB04109) associated with the musculoskeletal system useful
 CC for preventing, treating or ameliorating medical conditions e.g. by
 CC protein or gene therapy. The genes are isolated from a range of human
 CC tissues disclosed in the specification. The nucleic acids, proteins,
 CC antibodies and (ant)agonists are useful in the diagnosis, treatment
 CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
 CC other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences.
 XX
 SQ Sequence 5749 BP; 1600 A; 1192 C; 1403 G; 1553 T; 1 other;

Query Match 52.9%; Score 5724.8; DB 22; Length 5749;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 5740; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 4001 ATGGAAATCAACACAGCAAGGATGTGGAGAGGGGCGCTCACCTTCTCGAGGTG 4060
 DB 1 atggaaatcaacacacagcaaggtatgtggagaggggccccctccctcctgaggtg 60

QY 4061 TCAGAGCTTTTCATCTTTTCATCTTTTCATCTTTTCATCTTTTCATCTTTTCATCTTT 4120
 DB 61 tcagagcttttcattcttttcattcttttcattcttttcattcttttcattcttttcatt 120

QY 4121 GGGAGCAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4180
 DB 121 gggagcagggagagggagggagggagggagggagggagggagggagggagggagggaggg 180

QY 4181 GAAATAGGGACCTATTCTCTTTGGTGGCAGTTAAACAGGCTGGGATTTTCCAGAGTCCC 4240
 DB 181 gaaatagggaacctattctcttttgggtggcagtttaaacaggctgggattttccagagtc 240

QY 4241 ACACCTCGAGTCACTCTGGCTGTGAATTCAGAGAGACACAGTACCGAGGGCTACT 4300
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 DB 301 ggaagtacgggtatgatgggagggacaccttgaatttcgctccctgacacactggattgga 360

QY 4361 GAGCAGCAAGACCCAGGCGCTGGCCCAACAGCTGGAGTGGGAAGGCACAAAGATTCCGG 4420
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QY 4421 CCAGCAGAACAGGCGCTTACCTGAGAGGAGTCCCTGACAGCTGACAGTGTGCTGG 4480
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QY 4481 AGCTGGGAGAGGTGTTTGGACCAACAGGTATGGTGGAAACACTTCTGCCCTATA 4540
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QY 4781 TGTATATTTATACCTGTTAAATAATTCAGAAATGTCAGAGCGCGGACGGTGGCTCACCCC 4840
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QY 4841 TGTAAATCCCAGCACTTTGGGAGCGCGGAGGTGTGTACAAAGTTCAGAGTTCAGAGACC 4900
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QY 4901 AGCCTGACCAACATGGTGAACCCGCTCTTAAATAATACAAAAATAGTGTGTACAGT 4960
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QY 5201 AGGTTAAAAATTTTCATAGAACATAGCAATAATATCACTGAAGCTACCTATCTTACAAG 5260
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QY 5381 GATATGTATATTTACATGTGAGGAGACAGCTGATCTGACTGCTCTCAAGTGACACTG 5440
 DB 1380 gatgtatatttcatgtgaggagacaagctgactgctcctcaagtgacactg 1439

QY 5441 TGTTAGAGTCCAATCTTAGGACAAAAATGGTGTCTCTCTGTAGCTGTGTTTTTTCTCA 5500
 DB 1440 tgttagagtccaatcttaggacacaaaaatggtgtctctcctctgagcttcttcttcttga 1499

QY 5501 AAAGGATTTTCTCTCTCTCAACCTATAGAAGGAAGTGAAGTTCAGTCTTCTCTGGCAA 5560
 DB 1500 aaagggtatttctctctccaacctatagaaggaagtgaagttccagcttctcctgggaa 1559

QY 5561 GGGTAAACAGATCCCT 5620
 DB 1560 gggtaaacagatccccct 1619

xx Homo sapiens.
os WO9814466-A1.
xx 09-APR-1998.
xx 30-SEP-1997; 97WO-0517658.
xx 07-MAY-1997; 97US-0852495.
xx 01-OCT-1996; 96US-0724394.
xx (PROG-) PROGENITOR INC.
xx Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas WJ;
xx Tsuchihashi Z, Wolff RK;
xx WPI; 1998-240014/21.
xx Hereditary haemochromatosis gene products - used to develop products
xx for the diagnosis and treatment of hereditary disorders in iron
xx metabolism
xx Example 2; Fig 8; 209pp; English.
xx The present invention describes hereditary haemochromatosis gene
xx products from the human haemochromatosis gene. The present sequence
xx represents a hereditary haemochromatosis subregion from an individual
xx unaffected by hereditary haemochromatosis (HH). Also described is a
xx method to determine the presence or absence of the common hereditary
xx haemochromatosis (HFE) gene mutation in an individual comprising:
xx (a) providing DNA or RNA from the individual; and (b) assessing the
xx DNA or RNA for the presence or absence of a haplotype or genotype where
xx the presence or absence of the haplotype genotype indicates the likely
xx presence of the HFE gene mutation in the genome of the individual. The
xx HFE gene sequences from the present invention can be used to develop
xx products for use in the diagnosis and treatment of HFE. The present
xx invention also describes BTF genes, which are homologues of the milk
xx protein butyrophilin (BT), and can be used in the production of agonists
xx and antagonists of BT function. Also described are: (1) a Roret gene
xx which can be used to develop products for the study, diagnosis and
xx treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
xx which are homologues of a type 1 sodium transport gene, and can
xx similarly be used for hypophosphatemia.
xx Sequence 235033 BP; 69786 A; 48466 C; 49441 G; 68340 T; 0 other;
Query Match 28.7%; Score 3109; DB 19; Length 235033;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 10810; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 1 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAAATCATRAATATTTA 60
Db 47148 TCTAAGGTTGAGATAAAATTTTAAATGTATGATTGAATTTTGAAATCATRAATATTTA 47089
QY 61 AATATCTAAAGTTTCAGATCAGACATTCGGAACCTACTTTCCCAATCAACACCCCT 120
Db 47088 AATATCTAAAGTTTCAGATCAGACATTCGGAACCTACTTTCCCAATCAACACCCCT 47029
QY 121 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 180
Db 47028 TCAGGATTTAAAAACCAAGGGGACACTGGATCACCTAGTGTGTTTCAACAGCAGGTACCTT 46969
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTCTGAAAGACCTGTGTCCTTTTACCAGGAAGTT 240
Db 46968 CTGCTGTAGGAGAGAGAACTAAAGTCTGAAAGACCTGTGTCCTTTTACCAGGAAGTT 46909
QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGAGGCATCCCGG 300
Db 46908 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGACTTCTGAGGCATCCCGG 46849
QY 301 TTTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGGACGTGCGGCCAGAGCTGGGGAA 360

Db 46848 TTTTCCCGCCCCCAAAAGAGCGGAGATTTAAACGGGGACGTGCGGCCAGAGCTGGGAA 46789
QY 361 ATGGGCCCCGAGCCAGCCGCGCTTCTCCTCCTGATGCTTTTTCAGACCGCGGTCTCG 420
Db 46788 ATGGGCCCCGAGCCAGCCGCGCTTCTCCTCCTGATGCTTTTTCAGACCGCGGTCTCG 46729
QY 421 CAGGGCGCGTCTGCTCGTGAFTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 480
Db 46728 CAGGGCGCGTCTGCTCGTGAFTCCGAGGGCTGCGGGCGAACTAGGGGCGCGCGGGGTG 46669
QY 481 GAAAAATCGAAACTAGCTTTTCTTTGGCTTGGAGTTTGTAACTTTGGAGACCTGC 540
Db 46668 GAAAAATCGAAACTAGCTTTTCTTTGGCTTGGAGTTTGTAACTTTGGAGACCTGC 46609
QY 541 TCAACCCCTATCCGAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 600
Db 46608 TCAACCCCTATCCGAAGCCCTCTCCCTACTTTCTGCGTCCAGACCCCGTGAGGAGTGC 46549
QY 601 CTACCACCTGAACCTGCAGATAGGGTCCCTCGCCGCCAGACCTGCCCCCTCCCGGGCTGT 660
Db 46548 CTACCACCTGAACCTGCAGATAGGGTCCCTCGCCGCCAGACCTGCCCCCTCCCGGGCTGT 46489
QY 661 CCGGCTCTCGGGAGTGACTTTTGAACCGCCCACTCCCTTCCCGCCCACTAGAATGCTTT 720
Db 46488 CCGGCTCTCGGGAGTGACTTTTGAACCGCCCACTCCCTTCCCGCCCACTAGAATGCTTT 46429
QY 721 TAAATAAATCTCGTAGTTCCTCCTCCTGAGCTGAGTAAGCCTGGGGCTCCTTGAACCTGG 780
Db 46428 TAAATAAATCTCGTAGTTCCTCCTCCTGAGCTGAGTAAGCCTGGGGCTCCTTGAACCTGG 46369
QY 781 AACTCGGTTTATTTCCAAATGTCAGCTGTGAGTTTTTCCCGCAGTCAATCTCCAAACAGG 840
Db 46368 AACTCGGTTTATTTCCAAATGTCAGCTGTGAGTTTTTCCCGCAGTCAATCTCCAAACAGG 46309
QY 841 AAGTTCTTCCCTGAGTGTGCTGCCGAGAAGGCTGAGCAACCCACAGCAGGATCCGCACGG 900
Db 46308 AAGTTCTTCCCTGAGTGTGCTGCCGAGAAGGCTGAGCAACCCACAGCAGGATCCGCACGG 46249
QY 901 GGTTTCCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAGAGTGGCGTTGGGGA 960
Db 46248 GGTTTCCACCTCAGAACGAATGCGTTGGCGGTGGGGCGCGAAGAGTGGCGTTGGGGA 46189
QY 961 TCTGAATTTCTCACCATTCACCCACTTTTGGTGAGACCTGGGGTGGAGGTTCTTAGGGT 1020
Db 46188 TCTGAATTTCTCACCATTCACCCACTTTTGGTGAGACCTGGGGTGGAGGTTCTTAGGGT 46129
QY 1021 GGGAGGCTCCTGAGAGAGGCTACTCGGGCTTTTCCCGCACTCTTGCAATTTGTTCTTTT 1080
Db 46128 GGGAGGCTCCTGAGAGAGGCTACTCGGGCTTTTCCCGCACTCTTGCAATTTGTTCTTTT 46069
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Db 46068 GCCTGGAAAAATTAAGTATATGTTTGAACGTTTGAACGTTTGAACGTTTGAACGTTTGAACG 46009
QY 1141 CTAGCCTTTATGATTGCAATGCTGTGTAATTAAGAGCCCTCTCTACAAAGTACTGA 1200
Db 46008 CTAGCCTTTATGATTGCAATGCTGTGTAATTAAGAGCCCTCTCTACAAAGTACTGA 45949
QY 1201 TAATGAACATGTAAGCAATGCATCTTAAGTTACATTCATATCATGATCTTATTGA 1260
Db 45948 TAATGAACATGTAAGCAATGCATCTTAAGTTACATTCATATCATGATCTTATTGA 45889
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Db 45888 TTTTCACTAGGCATAGGAGGTAGSAGCTAATAATACGTTTATTTTACTAGAAGTTAACT 45829
QY 1321 GGAATTCAGATATATACTCTTTTCAGGTTTACAAGNACATAAATCTGGTTTCTG 1380
Db 45828 GGAATTCAGATATATACTCTTTTTCAGGTTTACAAGNACATAAATCTGGTTTCTG 45769
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTAATCTTAGTTGACAGTGAATTTTGGCCCTGTAG 1440

Db	45768	ATGTTATTCAAGTACTACAGCTGCTTCTAATCTTAGTTGACAGTGATTTGCCCTGTAG	45700
Qy	1441	TGTAGACAGTGTCTGTGGGTACACGCCGGCTCAGACAGCACTTTGAGTTTTGGTA	1500
Db	45708	TGTAGACAGTGTCTGTGGGTACACGCCGGCTCAGACAGCACTTTGAGTTTTGGTA	45649
Qy	1501	CTACGTGTATCCACATTTTACACATGACAAGATGAGCATGGCAGCGCTCTTCCTGG	1560
Db	45648	CTACGTGTATCCACATTTTACACATGACAAGATGAGCATGGCAGCGCTCTTCCTGG	45589
Qy	1561	CAAAATTATTCATCGGTACACTGGCTTTGGTGGCAGAGCTATGTCCTCCATTCATAGC	1620
Db	45588	CAAAATTATTCATCGGTACACTGGCTTTGGTGGCAGAGCTATGTCCTCCATTCATAGC	45529
Qy	1621	TATGATTCCTTAACATCACACTGCATTAGAGTTGAATATAAATTTTCATTTGAGCAG	1680
Db	45528	TATGATTCCTTAACATCACACTGCATTAGAGTTGAATATAAATTTTCATTTGAGCAG	45469
Qy	1681	AAATATTCAATCTTTTACAAGTGAATAGTCCAGCCAGCATGCTGTCACGTGTTCAAGCCC	1740
Db	45468	AAATATTCAATCTTTTACAAGTGAATAGTCCAGCCAGCATGCTGTCACGTGTTCAAGCCC	45409
Qy	1741	CAAGGAGAGAGCAGGGGAAAACAAGTCTTACCCTTTGATATTTTGCATTCAGTGGAGA	1800
Db	45408	CAAGGAGAGAGCAGGGGAAAACAAGTCTTACCCTTTGATATTTTGCATTCAGTGGAGA	45349
Qy	1801	GATGACAATAAGCAAAATGAGCAGAAAAGATATACAACATCAGGAAATCATGGGTGTTGA	1860
Db	45348	GATGACAATAAGCAAAATGAGCAGAAAAGATATACAACATCAGGAAATCATGGGTGTTGA	45289
Qy	1861	GAAGCAGACAAGTCAGGCAAGTCACACTCTGGGGCTGCACCTTGAGCAGAGACATCAAGGA	1920
Db	45288	GAAGCAGACAAGTCAGGCAAGTCACACTCTGGGGCTGCACCTTGAGCAGAGACATCAAGGA	45229
Qy	1921	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCCAAACTGAGTGGGCTGGCAAG	1980
Db	45228	AATAAGAAATGATATTGACTGGGAGCAGTATTTCCAGGCCAAACTGAGTGGGCTGGCAAG	45169
Qy	1981	TTGGATTAAAAAGCCGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGGGG	2040
Db	45168	TTGGATTAAAAAGCCGGTTTTCTCAGCACTACTCATGTGTGTGTGGGGGGGGGGGG	45109
Qy	2041	CGCGTGGGGTGGGAAGGGGCACTACCATCTGCATGTAGGATGCTACGAGTATCCGT	2100
Db	45108	CGCGTGGGGTGGGAAGGGGCACTACCATCTGCATGTAGGATGCTACGAGTATCCGT	45049
Qy	2101	CCTCCCTACTACTAGTGTCTAGGAGCACTCCCCAGCTCTTGACAACAAAATGTCTCT	2160
Db	45048	CCTCCCTACTACTAGTGTCTAGGAGCACTCCCCAGCTCTTGACAACAAAATGTCTCT	44989
Qy	2161	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA	2220
Db	44988	AAACTTTGCCACATGTCACCTAGTAGACAAACTCCTGGTTAAGAAGCTCGGGTTGAAAA	44929
Qy	2221	AATAACAAGTAGTCTGGGAGTAGAGGCCACAGAAGTAGGTAAATGGCTCAGAGAGGA	2280
Db	44928	AATAACAAGTAGTCTGGGAGTAGAGGCCACAGAAGTAGGTAAATGGCTCAGAGAGGA	44869
Qy	2281	GCCAACAAACAGGTTGTGACGCGCTGTAGGCTGTGGTGTGAATTTCTACCCAAGAGTA	2340
Db	44868	GCCAACAAACAGGTTGTGACGCGCTGTAGGCTGTGGTGTGAATTTCTAGCCAAGAGTA	44809
Qy	2341	ACAGTGATCTGTACAGAGCTTTTAAAGATTGCTCTGGCTGCTATCTGGAAGACAGATG	2400
Db	44808	ACAGTGATCTGTACAGAGCTTTTAAAGATTGCTCTGGCTGCTATCTGGAAGACAGATG	44749
Qy	2401	AAGGGAGCAACAGTAAAGCAGGGGCCAGCAGGAAGCTGTTACACAGTCCAGCAAG	2460
Db	44748	AAGGGAGCAACAGTAAAGCAGGGGCCAGCAGGAAGCTGTTACACAGTCCAGCAAG	44689
Qy	2461	AGGTAGTGGAGTGGCTGGGTGGGAACAAAGAGGAGTGACAAACCATTTGCTCCTGAA	2520
Db	44688	AGGTAGTGGAGTGGCTGGGTGGGAACAAAGAGGAGTGACAAACCATTTGCTCCTGAA	44629

QY 3601 ACCAGGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCCAAATAAGGGA 3660
Db 43549 ACCGAGACTGTCATATGGAAGAAAGACAGGACTGCAACTCACCCCTTCCAAATAAGGGA 43490
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QY 3721 CTCCTACTACACATGGTTAAGGCCCTGTGTCTGTCTCTCCAGAGTTCACACTCTCTGCACTA 3780
Db 43429 CTCCTACTACACATGGTTAAGGCCCTGTGTCTGTCTCTCCAGAGTTCACACTCTCTGCACTA 43370
QY 3781 CCTCTTCATGGGTGCTCAGACAGGACCTTGCTCTCTCTGTTGAGCTTTGGGCTA 3840
Db 43369 CCTCTTCATGGGTGCTCAGACAGGACCTTGCTCTCTCTGTTGAGCTTTGGGCTA 43310
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Db 43309 CTTGGATACACAGCTGTTCTGTTCTATGATCATGAGAGTGCCTGTTGGAGCCCGAAC 43250
QY 3901 TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAAGTGCAGAGTCTGAA 3960
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QY 4021 CAAGGTATGTGGAGAGGGGCCCTCACCTTCCCTGAGGTTGTGAGAGCTTTTCATCTTTTC 4080
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QY 4081 ATGCATCTTGAAGGAAACAGCTGGAAGTCTGAGGTCTTGTGGAGCAGGGAAGGGGAAG 4140
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Db 42949 TGGTTGCAGTTAAACAGGCTGGGATTTTTCCAGAGTCCCAACACCCCTGCAGTCTATCTG 42890
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QY 5161 ATATCAAGTGAAGGCTTATCAGAGTGAAGAAATCTTTAGGTTAAAGTTCTTTCAT 5220
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Db 40189 TTCAGATGAGAGATAATAGTTCTTTGAAATCCCAATAGTGTCCCAAGGTCTAAATTTGAGATGG 40130
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QY 421 CAGGGCGCTTGCCTGCGTGAGTCCGAGGGCTGCGGGCGAAGTACGGGGCGCGGGGGTG 480

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QY 481 GAAAAATCGAACTAGCTTTTCTTTGGCGCTTGGAGTTTCTTAACCTTTTGAGGACCTGC 540

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QY 541 TCAACCCCTATCCGGAAGCCCTCTCCCTACTTTCTGGTCCAGACCCCGTGAGGAGTGC 600

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PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.

PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249266.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-451937/48.
XX
DR Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the musculoskeletal system including
PT musculoskeletal cancers and also for testing and detection e.g.
PT diagnosis -
XX
PS Example 2; SEQ ID NO 3113; 781pp + Sequence Listing; English.
XX

CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABR03087-ABR04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1712 BP; 487 A; 361 C; 375 G; 489 T; 0 other;

Query Match 15.8%; Score 1712; DB 22; Length 1712;
Best Local Similarity 100.0%; Pred. No. 2.3e-291;
Matches 1712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8039 TACATGCATTACTGCATGCATCTTTTACAATAATCTATGAGATAGGTACTATTATCCCC 8098
Db 1 tacatgcattactgcactgcacttcttacaataatctatgagataggtactattatcccc 60
QY 8099 ATTTCTTTTAAATGAAGAAAGTAGTCAGCCGGCAGCGTGGCTCACCGCTGTAATC 8158

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|||||
Db 61 attctttttaataagaagaagtgaagtaggcccgggacggtggctccgcgcgcaac 120
QY 8159 CCAGCACTTTGGGAGGCCAAAGCGGTGGATCAGAGGTCAGAGATCGAGACCATCTCTG 8218
Db 121 ccagcaactttgggagcccaaaagcggtggatcacgaggtcagagatcgagaccactcg 180
QY 8219 GCTAACATGTTGTAACCCCAATCTCTAATAAAAAATACAAAAATTTAGCTGGCGTGGTGGC 8278
Db 181 gctlaacatgggtaaacccccctctctaataaaaaatacaaaaaattagctggcggtggcg 240
QY 8279 AGAGCCCTGTGAGTCCCAAGCTACTCGGAAGGCTGAGGCGAGGAGATGGCATGAACCCAGGA 8338
Db 241 agacgctctgagtcctccagctcactcggaggtgagcgagggagaaatgagcgaaccagga 300
QY 8339 GGCAGAGCTTTGCAGTGAGCCGAGTTTGGCCCACTGACACTCCAGCTGAGTGACAGAGTGA 8398
Db 301 ggcagagcttgagtgagcgaggtttgcccactgcaactcagcctcaggtgacagagtgga 360
QY 8399 GACTCCATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 8458
Db 361 gactcccatctcaaaaaataaaaaataaaaaataaaaaataaaaaataaaaaataaaaaa 420
QY 8459 TATAGAGTATCTCATAGTTTGTCACTAGTATAGAAACAGGTTTCAAACTCAGTCAATCTGAC 8518
Db 421 tatagatatctcatagtttgctcagtgatagaaacaggtttcaaaactcagtcgaactgac 480
QY 8519 CGTTTGATACATCTCAGACACCACTACATTCAGTAGTTTATAGTCCCTAGATTAATAGAG 8578
Db 481 cgtttgatcatctcagacacacacacacacacacacacacacacacacacacacacacac 540
QY 8579 AAGGAAGGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8638
Db 541 aaggaaaggagatggctctctctctctctctctctctctctctctctctctctctctctct 600
QY 8639 ATGAAGGGGAACAGCAGAAAAACAACTGATCTCAGCTGCTCATGTTTCTCTTTTAAAG 8698
Db 601 atgaaggggaacagcagaaaaacaaacacacacacacacacacacacacacacacacac 660
QY 8699 TCCCTGAAGGAGGTCTCTGGAAATGTGACTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8758
Db 661 tccctgaaggaggtctctgggaatgtgactccctctgctccctctgctctctctctctctct 720
QY 8759 CATTTCTTTGGACCTACGCAAGGACTGAATTTGGTGGGACAGCTAGTGGCCCTGCTGG 8818
Db 721 cattctttggaccctacgcaaggactgaatgtgtgggacagctagtgccctgctgg 780
QY 8819 GCTTCACACACGGTGTCTCTCCCTAGGCCAGTGCCTCTGGAGTCAAGACTCTGGTGGTATT 8878
Db 781 gcttcacacacggtgtctctccctagggccagtgccctgagagcagaactctggtggtatt 840
QY 8879 TCCCTCAATGAAGTGGAGTAAAGCTCTCATTTTGGATGCTATAATGGAAGCCACCAAG 8938
Db 841 tccctcaatgaagtggagtaagctctctctcaatttgagatggataataaggaaagccacca 900
QY 8939 TGGCTTAGAGGATGCCAGGCTCTTCCATGAGGCCACTTGGGGTTCGGGTGCACATTAATA 8998
Db 901 tggcttagagatgccaggtctctccatggagccactggggttccgggtgcacattaaaa 960
QY 8999 AAAAAATCTAACCGACATTCAGGAATTTAGATTCTGGGAATCAGTTTCAACCATGTT 9058
Db 961 aaaaaatctaacacagcattcagggaattgttagattctgggaaatcagttcaccagtt 1020
QY 9059 CAAAAGAGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 9118
Db 1021 caaaagagctctctctctctctctctctctctctctctctctctctctctctctctctct 1080
QY 9119 ATCTCGGCTCACTGAACCTCTGCTCCAGGTTCAACGATTCCTCTGCTCAGCCCTCC 9178
Db 1081 atctcggtcactgtaacctctgctccagggttcaagcgaattctcctgctcagcctcc 1140
QY 9179 CAAGTAGCTGGATTACAGGCGTGCACCACCATGCCCGCTAAATTTTGTATTATTAGTA 9238
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Db 1141 caagtagctgggattaccaggcggtgcaaccacatgcccgggctaatttttatttttagta 1200
QY 9239 GAGACAGAGGTTTACCATTTGTTGGCCAGGCTGGTCTCGAAGCTCTCTGACCTCGTATCCG 9298
Db 1201 gagacaggggtttcacatgttggccagggtgtctcgaactctcctgacctcgtgatccg 1260
QY 9299 CQTGCTCGGCTCCCAAGTCTGAGATTACAGTGTGAGCCACCTGCGCCAGCCGTCA 9358
Db 1261 cctgctcggccctcccaaaagtgtgagattacaggtgtgagccacctgcccagccgta 1320
QY 9359 AAAAGTCTTAATATATATATATATATATATATATATATATATATATATATATATATATAT 9418
Db 1321 aaagagtcttaataataataataataataataataataataataataataataataataata 1380
QY 9419 TGCCTGCATAAATGTGTTACAGCATTTCTGCTTCAAGGCGAGGCTTCAGGATACCAT 9478
Db 1381 tggctgcataaaatgttgcacagcattctgtcttgaaaggcaggtgtctcagggataccat 1440
QY 9479 ATACAGCTCAGAAAGTTCTTTTAGGCATTAATTTTAGCAAGATATCTCATCTCTTTC 9538
Db 1441 atacagctcagaagttctctctctctctctctctctctctctctctctctctctctct 1500
QY 9539 TTTTAAACCATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 9598
Db 1501 ttttaaacattctctctctctctctctctctctctctctctctctctctctctctctctct 1560
QY 9599 TTACGCTCATTTGTAGAAAAGCTATAAATGAATACAAATTAAGCTGTATTATTAATAGCC 9658
Db 1561 ttacgctcattgtagaaaagctataaaatgaatacaattaaagcgttatttaattagcc 1620
QY 9659 AGTGAAAAACTATTACAACTTGTCTATTTACCTGTTAGTATTATTGTCGCATTAATAATG 9718
Db 1621 agtgaaaaactattaaacaactgtctattaccctgttagtattattgttgctataaaatg 1680
QY 9719 CATATACTTTTAATAATGTATATTGTATTGTA 9750
Db 1681 catatacttaataaatgtattgtattgta 1712

RESULT 13
AA96769
ID AAA96769 standard; cdna; 2506 BP.
XX
AC AAA96769;
XX
DT 19-FEB-2001 (first entry)
XX
DE cdna sequence encoding a histocompatibility iron loading (HFE) protein.
XX
KW Human; histocompatibility iron loading protein; HFE protein;
KW major histocompatibility complex; non-classical class I gene;
KW chromosome 6p; iron disorder; haemochromatosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1044
FT /tag= a
FT /product= "histocompatibility iron loading (HFE) protein"
FT sig_peptide 1..66
FT /tag= b
FT mutation 187
FT /tag= c
FT /note= "if this base is mutated to G, then the
FT protein contains the mutation H63D"
FT mutation 193
FT /tag= d
FT /note= "if this base is mutated to T, then the
FT protein contains the mutation S65C"
FT mutation 277
FT /tag= e
FT /note= "if this base is mutated to C, then the
FT protein contains the mutation G93R"

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FT mutation 314
FT /**tag= f
FT /note= "if this base is mutated to C, then the
FT protein contains the mutation I105P, which
FT is associated with an iron overload disorder"
PN WO200058515-A1.
XX 05-OCT-2000.
PD 24-MAR-2000; 2000WO-US07982.
XX 26-MAR-1999; 99US-0277457.
PR (BILL-) BILLUPS-ROTHENBERG INC.
XX Rothenberg BE, Sawada-Hirai R, Barton JC;
XX WPI; 2000-647244/62.
DR P-PSDB: AAB19149.
XX
XX Diagnosing an iron disorder e.g. hemochromatosis or a genetic
PT susceptibility to develop it, by determining the presence of a mutation
PT in exon 2 or an intron of a histocompatibility iron loading nucleic
PT acid -
XX
PS Disclosure; Page 2-3; 55pp; English.
XX
CC The present sequence encodes a human histocompatibility iron loading
CC (HFE) protein. The HFE gene is a major histocompatibility (MHC)
CC non-classical class I gene located on chromosome 6p. Mutations in the
CC gene lead to iron disorders. The specification describes a method for
CC diagnosing an iron disorder or a genetic susceptibility to develop the
CC a mutation in a mammal. The method comprises determining the presence of
CC a mutation in exon 2 or an intron of a HFE gene or protein. The mutation
CC is not a C to G missense mutation at nucleotide 187 of the sequence
CC given in A96769 (Genbank Accession number U60319). The presence of the
CC mutation indicates the disorder or the genetic susceptibility to the
CC disorder. The method is used to diagnose an iron disorder
CC e.g. haemochromatosis, or a genetic susceptibility to develop it.
XX
XX Sequence 2506 BP; 648 A; 552 C; 596 G; 710 T; 0 other;

Query Match 9.7%; Score 1051.6; DB 21; Length 2506;
Best Local Similarity 98.7%; Pred. No. 1.8e-175;
Matches 1060; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 7104 CAGGAGGAGCCATGGGCACTACGCTTGTAGCTGAAGCTGAGTGACACGCGCTGCAGAC 7163
|| |||||
Db 1004 caagaggagccatgggacctactgctttagctgaacgtgagtgacacgcagcctgcagac 1063
|| |||||
QY 7164 TCACTGTGGGAAGGAGACAAAACATAGAGACTCAAGAGGGAGCTGCATTTATGAGCTCTTC 7223
|| |||||
Db 1064 tcactgtgggaagagagacaaaactagactcaaaagaggagtgctattatgagctcttc 1123
|| |||||
QY 7224 ATGTTTCAGGAGAGCTGACCTTAACATAGAAAATGGCTGACGACCTCCTTGATTTTA 7283
|| |||||
Db 1124 atgtttcagagagaggtgaacctaaacataaataatgctgacgaacctcctgatttta 1183
|| |||||
QY 7284 GCCTTCTCTGTTTCATTTTCCTCAAAAAGATTTCCTCCATTTAGGTTTCTGAGTTTCTTGCATG 7343
|| |||||
Db 1184 gccttctctgttcattctcctcaaaaagatttccccatttaggtttctgagttcctgcagtg 1243
|| |||||
QY 7344 CCGGTGATCCCTAGCTGTCGACCTCTCCCTGGAACGTGCTCTCATGAACTCAAGCTGCA 7403
|| |||||
Db 1244 ccggtgatccctcagctgtgacctctccctggaaactgtctcatgaacctcaagctgca 1303
|| |||||
QY 7404 TCTAGAGGCTTCTCTCATTTCTCTCCGTCACCTCAGAGACATACACCTATGTCATTTTCAT 7463
|| |||||
Db 1304 tctagaggttcttctcattctcgttcacctcagagacatacacctatgtcatttcatt 1363
|| |||||
QY 7464 TCCATTTTGGAGAGGAGACTCCTTAAATTTGGGGGACTTACATGATTCATTTTAACATC 7523

Db 1364 tccatttttggaaaggagacctccttaaatcttgggggaacttacatgattcattttaacatcc 1423
|| |||||
QY 7524 TGAGAAAAGCTTTGAACCCCTGGGACGTGGCTAGTATACATAACCTTACCAGATTTTACACAT 7583
|| |||||
Db 1424 tgagaaaagctttgaacccttgggacgtggctagtcataaaccctaccagatttttacacat 1483
|| |||||
QY 7584 GATCTATGCATTTTCTGGACCCGTTCAACTTTTCTTGAATCTCTCTCTGTGTGTACC 7643
|| |||||
Db 1484 gatatcatgcatcttcttgaccccgcttcaactttctcttgaatcctctctctctgtgttacc 1543
|| |||||
QY 7644 CAGTAACCTCATCTGTCAACAAGCCTTTGGGGATTCTTCATCTGATTTGTGATGTGAGTTGC 7703
|| |||||
Db 1544 cagtaactcatctgtcaccacaccccttggggatctctccatctgattgagtgagtgc 1603
|| |||||
QY 7704 ACAGCTATGAAGGCTGTACACTGCACGAATGAAGAGGCACCTGTCCCAGAAAAAGCATC 7763
|| |||||
Db 1604 acagctatgaaggctgtgcactgacgaatggaagaggcacctgtccccagaaaaagcatc 1663
|| |||||
QY 7764 ATGGCTATCTGTGGGTAGTATGATGGGTGTTTTTAGCAGGTAGGAGGCAAAATATCTTGAA 7823
|| |||||
Db 1664 atggctatctgtgggttagttagtggtgttttagcaggttagggaggaataatctgtgaa 1723
|| |||||
QY 7824 AGGGGTTGTGAAGAGGTGTTTTTCTAATTGGCATGAAGGTGTCATACAGATTTTGCAAAG 7883
|| |||||
Db 1724 aggggtgtgaaagaggtgttttttctaatggcatgaagggtgcatcacagatttgcaag 1783
|| |||||
QY 7884 TTATATGGTGCCCTTCATTTGGGATGCTACTCTAGTATTTCCAGACCTGAAGAATCACAAATA 7943
|| |||||
Db 1784 tttaatgtgtgcttcttatttggatgctactctctagttattccagacctgaagaatcacata 1843
|| |||||
QY 7944 ATTTTCTACCTGGTCTCTCCTTGTGTTCTGATTAATGAAATTTATGATAAGGATGATGATAAGC 8003
|| |||||
Db 1844 atttctaccgtgtctctctgttctgataataatgaaaattatgataaggaTgataaaagc 1903
|| |||||
QY 8004 ACTTACTTCGTGTCGACTCTTCTGAGCACCTTACTACATGCATTTACTGTCATGCACTTCT 8063
|| |||||
Db 1904 acttactctgtctcgcactctctcgcacacttacttactacatgcattactgcacttct 1963
|| |||||
QY 8064 TACAATAATTTCTATGAGATAGGTACTATTATCCCATTTCTTTTAAATCAAGAAAAGTG 8123
|| |||||
Db 1964 tacaataattctatgagataggtactattatccccattcttctttaaataagaagaagtg 2023
|| |||||
QY 8124 AAGTAGCCGGGACGCGTGGCTCAGCCTGTAAATCCCAAGCACTTTTGGGAGGCCA 8177
|| |||||
Db 2024 aagtagcggggcacggtggctcgcgctgtggtccccaggtgctgagattgca 2077
|| |||||

RESULT 14
AAV23525
ID AAV23525 standard; mRNA; 2727 BP.
XX
AC AAV23525;
XX
DT 10-JUL-1998 (first entry)
XX
DE Haemochromatosis gene.
XX
KW Hereditary haemochromatosis; HC gene; HH identification; diagnosis;
KW autosomal recessive disorder; ss.
XX
OS Homo sapiens.
XX
FN WO9807884-A1.
XX
PD 26-FEB-1998.
XX
PF 22-AUG-1997; 97WO-AU00539.
XX
PR 03-SEP-1996; 96AU-0002083.
PR 23-AUG-1996; 96AU-0001849.
XX
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX Busfield F, Cullen LM, Jazwinska EC, Powell LW;
PI WPI: 1998-179064/16.
XX Detection of autosomal recessive disorder - particularly hereditary
PT haemochromatosis, by detecting a mutation in the HC gene
XX
PS Disclosure; Page -: 32pp; English.
XX
CC This sequence represents the haemochromatosis (HC) gene. Mutations in
CC this sequence are detected using the method of the invention. The method
CC is for identifying an individual with hereditary haemochromatosis (HH) or
CC a predisposition to develop HH or to genetically pass on HH to an
CC offspring, comprising isolating a biological sample and amplifying a
CC region of genomic DNA in the biological sample encompassing all or part
CC of the DNA between markers D6S265 and D6S276, and detecting at least one
CC homozygous or heterozygous mutation in a nucleotide within the region.
CC The method can also be used for identifying an individual with an
CC autosomal recessive disorder (ARD) or predisposition to develop and/or
CC genetically pass on an ARD to an offspring, comprising isolating a
CC biological sample from the individual and screening genomic DNA in the
CC sample for the presence of a homozygous or heterozygous mutation in a
CC gene, the normal function of which, is required to prevent progression of
CC the disorder. The method(s) can be used to identify individuals that are
CC homozygous or heterozygous (carriers) for the mutation causing the ARD.
CC Especially the method is used to diagnose HH or predisposition to HH by
CC detecting a Cys282Tyr substitution. Individuals homozygous for this
CC mutation have HH and heterozygotes are potential carriers of the
CC disease.
XX
SQ Sequence 2727 BP; 702 A; 606 C; 560 G; 759 T; 0 other;

Query Match 9.7%; Score 1051.6; DB 19; Length 2727;
Best Local Similarity 98.7%; Pred. No. 1.9e-175;
Matches 1060; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 7104 CAGGAGGAGCCNTGGGACACCTACGCTCTAGCTGACGTGACAGGAGCGCTGACGAC 7163
DB 1225 caagagagccatggggcactacgtcttagctgaacgtgagtgacacgcagcgcgcagac 1284
QY 7164 TCACCTGTGGGAGGAGACAAACCTAGAGACTCAAGAGGGAGTGCAATTTATGAGCTCTTC 7223
DB 1285 tcaactgtgggaagagacaaactagagactcaagaggagtgatattatgagctcttc 1344
QY 7224 ATGTTTCAGGAGAGGTTGAACCTTAACATAGAAATTCCTCGAGCACTCCTTGATTTTA 7283
DB 1345 atgtttcagagagagagtggaacctaaacatagaaattgcctgacgaactccttgattta 1404
QY 7284 GCCTTCTCTGTTCATTTCTCTCAAAAAGATTTCCCATTTAGGTTTCTGAGTTCCTGCATG 7343
DB 1405 gctctctctgttcattctcctcaaaaagattccccattagggttctgagttcctgcagt 1464
QY 7344 CCGGTGATCCCTPAGCTGTGACCTCTCCCTCGAACTGTCTCTCATGAACCTCAAGCTGCA 7403
DB 1465 ccggtgatccctagctgtgacctctccctctggaactgtctctcatgaacctcaagctgca 1524
QY 7404 TCTAGAGGCTTCCTTCATTTCTCTCGTCACCTCAGACATACACCTATGTCATTTTCATT 7463
DB 1525 tctagaggtctctctcattctcctcgctcagctcagagacaacacacctatgctcattcatt 1584
QY 7464 TCCTATTTTGGAGAGGAGGACCTCTTAATTTTGGGGGACTTACATGATTCATTTTAACATC 7523
DB 1585 tctatttttggagaggagactccttaaatitgggggacttacatgattcatttttaacatc 1644
QY 7524 TGAAGAAAGCTTTGAACCTGGAGCGTGGCTAGTCATACACCTTACCAGATTTTACACAT 7583
DB 1645 tdagaaaagctttgaaacctgggacgtgctagtcataaacctaccagattttttacacat 1704
QY 7584 GTATCTATGCATTTTCTGGACCGCTCAACTTTTCCCTTTGAATCCTCTCTCTGTGTACC 7643
DB 1705 gtatctatgcatcttctgagaccggttcaacttttccctttgaaatcctctctctgtgtacc 1764

QY 7644 CAGTAACCTCATCTCTCCACCAAGCCTTGGGATCTTCCATCTGATGTGATGTGCTGC 7703
DB 1765 cagtaacctcatctctgcccacgaagccttgggattcttccatctgattgtgatgctgctgc 1824
QY 7704 ACAGCTATGAAGGCTGTACACTGCACGAATGAAGAGGACCTGTCTCCAGAAAAGCATC 7763
DB 1825 acagctatgaaggtgtgctgactgcacgaatggaagaggcactgtcccagaaaaagcatc 1884
QY 7764 ATGGCTATCTCTGGGTAGTATGATGGGTGTTTACAGGTAGGAGGCAAAATATCTTGA 7823
DB 1885 atggctatctgtgggttagtatgaggtgttttttagcaggtaggagcacaatatcttgaa 1944
QY 7824 AGGGCTTGTGAAGAGGTGCTTTTCTTAATGGCATGAAGGTGTCATACAGATTTGCAAA 7883
DB 1945 aggggtgtggaagaggtgttttttctaattggcatgaaggtgcatcacagatttgcaga 2004
QY 7884 TTTAATGGTGCTTCATTTGGGATGCTACTCTAGTATTCAGACCTGAGAGATCACAAATA 7943
DB 2005 tttaatggcttctcatttgggatgctactctagttccagacacctgaagaatcacata 2064
QY 7944 ATTTCTACCTGGTCTCTCTCTTGTCTGATAAATAATATGATAGGATGATAAAGC 8003
DB 2065 attttctacctgtctctcctgttctgataatgaaattatgataagatgataaagc 2124
QY 8004 ACTTACTTCTGTGCTCGACTCTTCTGAGCAGCTACTTACTACATGCAATTTACTGCACTTCT 8063
DB 2125 acttacttctgtcgcactcttctgacacactactacattcatgctactgctgctctct 2184
QY 8064 TACATAATTTCTATGAGATAGTACTATTATCCCATTTCTTTTAAATGAAGAAAGTG 8123
DB 2185 tacaataattctatgataaggtactattatccccattctcttttttaaatgaagaagtg 2244
QY 8124 AAGTAGGCGGCGACGGTGGCTCACGCTGTGTAATPCCAGACCTTTTGGGAGGCCA 8177
DB 2245 aagtaggcggggcaggtggctgcgcctgtgtgtcccgagggtgctgagattgca 2298
RESULT 15
AAC68440
ID AAC68440 standard; DNA; 517 BP.
XX AAC68440;
XX
XX 21-FEB-2001 (first entry)
XX Human hereditary hemochromatosis DNA used for mutation detection.
DE HH; hereditary hemochromatosis; chelation agent;
KW T-cell differentiation factor; iron overload; ss.
XX Homo sapiens.
XX OS
XX US6140305-A.
XX
XX 31-OCT-2000.
XX
XX 04-APR-1997; 97US-0834497.
XX
XX 04-APR-1996; 96US-0630912.
XX 16-APR-1996; 96US-0632673.
XX 23-MAY-1996; 96US-0652265.
XX
XX (BIRA) BIO-RAD LAB INC.
PI Thomas WJ, Drayna DT, Gnirke A, Ruddy D, Tsuchihashi Z, Wolff RK;
PI Feder JN;
XX
XX WPI: 2001-006341/01.
XX
PT New hereditary hemochromatosis gene products or polypeptides, useful
PT for treating hereditary hemochromatosis in a patient, and as a metal
PT chelation agent alleviating iron overload -

oligo(4T) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. This library is the normalized version of NCI CGAP Brl.1. Library was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 132 a 107 c 107 g 107 t

ORIGIN

Query Match 3.7%; Score 404.6; DB 9; Length 453;
Best Local Similarity 98.8%; Pred. No. 3.1e-47;
Matches 418; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

8670 ATCTCAGCTGTCATGTTTCTTTAAAGTCCCTG-AAGGAAGTCTGGAATGTACTC 8728
|||||
453 ATCTCAGCTGTCATGTTTCTTTAAAGTCCCTGAAAGGAAGTCTGGAATGTACTC 394
|||||
8729 CCTTGTCTCTGTTGCTCTCTTTGGCATTCATTTCTTTGGACCTACGCAAGCATGTA 8788
|||||
393 CCTTGTCTCTGTTGCTCTCTTTGGCATTCATTTCTTTGGACCTACGCAAGCATGTA 334
|||||
8789 ATTGGGGGAGACGTAAGTGGGCTGCGGCTTCACACAGGCTGCTCCCTAGGCCAG 8848
|||||
333 ATTGGGGGAGACGTAAGTGGGCTGCGGCTTCACACAGGCTGCTCCCTAGGCCAG 274
|||||
8849 TCCCTCTGTGAGTCAGACACTGTGTGTATTTCCCTCAATGAAGTGAAGTCTCTCA 8908
|||||
273 TCCCTCTGTGAGTCAGACACTGTGTGTATTTCCCTCAATGAAGTGAAGTCTCTCA 214
|||||
8909 TTTTGAGATGTAATGAGAGCCCAAGTGGCTTAAGAGATGCCAGGTCTTCCATG 8968
|||||
213 TTTTGAGATGTAATGAGAGCCCAAGTGGCTTAAGAGATGCCAGGTCTTCCATG 154
|||||
8969 GAGCCACGTGGGTCCGGGTCACATTAATAAATAATCAACAGACATTCAGGAATG 9028
|||||
153 GAGCCACGTGGGTCCGGGTCACATTAATAAATAATCAACAGACATTCAGGAATG 94
|||||
9029 CTAGATTTGGGAAATCAATTCACCATGTTCAAAAGAGTCTTTTCTTTTGGAGAT 9088
|||||
93 CTAGATTTGGGAAATCAATTCACCATGTTCAAAAGAGTCTTTTCTTTTGGAGAT 34
|||||
9089 CTA 9091
|||
33 CCA 31

RESULT 15
A1160732/c 457 bp mRNA linear EST 26-OCT-1998
LOCUS A1160732
DEFINITION gba9b10.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1703419 3'
similar to contains Alu repetitive element; contains element MSR1
repetitive element ;, mRNA sequence.
ACCESSION A1160732
KEYWORDS A1160732.1 GI:3694112
SOURCE EST.
ORGANISM human.
Human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 457)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 876 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 399.
Location/Qualifiers

FEATURES

source

1. 457

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:1703419"

/clone_lib="NCI_CGAP_Brn23"

/tissue_type="glioblastoma (pooled)"

/lab_host="DH10B"

/note="Organ: brain; Vector: p7T3D-Pac (Pharmacia) with a

modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(4T) primer [5',

TGTTCACCAATCTGAAGTGGGAGCGGCGCATATCTTTTCTTTTCTTTTCTTTT

T 3']; double-stranded cDNA was ligated to Eco RI

adaptors (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of the modified p7T3 vector.

Library is normalized, and was constructed by Bento

Soares and M.Fatima Bonaldo."

BASE COUNT 104 a 144 c 100 g 109 t

ORIGIN

Query Match 3.6%; Score 393.8; DB 9; Length 457;
Best Local Similarity 91.8%; Pred. No. 1e-45;
Matches 416; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

7984 ATGATTAAGATGATTAAGAAGACATCTACTTCTGTCGCCACTCTTGAAGCACCTTACAT 8043
|||||
457 ATGATTAAGATGATTAAGAAGACATCTACTTCTGTCGCCACTCTTGAAGCACCTTACAT 398
|||||
8044 GCATTACTGCATGCATCTTCTTAATATTTCTATGATATGATATTTATCCCATTTTC 8103
|||||
397 GCATTACTGCATGCATCTTCTTAATATTTCTATGATATGATATTTATCCCATTTTC 338
|||||
8104 TTTTAAATGAAGAAGTGAAGTAGAGCCGCGGACAGGTGCTCAGCGCTTAATCCACAG 8163
|||||
337 TTTTAAATGAAGAAGTGAAGTAGAGCCGCGGACAGGTGCTCAGCGCTTAATCCACAG 278
|||||
8164 ACTTTGGAGGCCAAACGGGTGATCAGAGTCAAGATCGAAGCAATCCTGGCTTA 8223
|||||
277 ACTTTGGAGGCCGCGGGGTGATCGCAGAGTCAGAGATCGGGGCGCTCTGCTTA 218
|||||
8224 CATGTGAACCCCATCTCTAATATAAATAATTAAGTGGGCTGTGGCAGAGC 8283
|||||
217 CATGTGAACCCCGCTCTGTATTAAGATACGAAGAATTGGCTGGGCTGTGGGCGG 158
|||||
8284 CCTGTAGCCAGTACTCGGAAGCTGAGGACAGAGATGCGATGAACCCAGAGGACAG 8343
|||||
157 CCTGTAGCCAGTACTCGGAAGCTGAGGACAGAGATGCGATGAACCCAGAGGACAG 98
|||||
8344 AGCTTGCATGAGCGGATTTCCGCCATCGACTCCAGCCTAGGTGACAGATGAGACTC 8403
|||||
97 AGCTTGCATGAGCGGATTTCCGCCATCGACTCCAGCCTAGGTGACAGATGAGACTC 38
|||||
8404 CATCTCAAAAAAATAAATAAATAAATAAATAA 8436
|||||
37 CATCTCAAAAAAATAAATAAATAAATAAATAA 5

Search completed: June 19, 2002, 16:35:28
Job time: 11070 sec

QY	8847	AGTCCCTCTGGATCAGAACTCGGGGATATTCCCTCAATGAAGTGAGATAGCTCTG	8906
Db	345	AGTCCCTCTGGATCAGAACTCTGGGGATTTCCCTCAATGAAGTGAGATAGCTCTCT	286
QY	8907	CATTTCAGATGATATTAATGAAAGCCACCAGTGGCTTAGAGATGCCAGGTCCTTCCA	8966
Db	285	CATTTCAGATGATATTAATGAAAGCCACCAGTGGCTTAGAGATGCCAGGTCCTTCCA	226
QY	8967	TGGAG-CCAACTGGGGTCCGGGTGCACATTAATAAAAAATATAACCGAGGCAATTCAGGAA	9225
Db	225	TGGAGGCCCAATGGGGTCTCCGGGTGCACATTAATAAAAAATATAACCGAGGCAATTCAGGAA	166
QY	9026	TTGCTAGATTCTGGAAATCAGTTCACCATGTTCAAAGAGTCT-TTTTTTTTTTTTTTGA	9084
Db	165	TTGCTAGATTCTGGAAATCAGTTCACCATGTTCAAAGAGTCTTTTTTTTTTTTTTTGA	106
QY	9085	GACTCTATTGCCAGGCGTG 9103	
Db	105	GACTCTATTGCCAGGCGAG 87	

RESULT	13		
LOCUS	A0111002/c		
DEFINITION	A0111002 443 bp DNA linear GSS-29-AUG-1995 CIT-HSP-2370L14.TR CIT-HSP Homo sapiens genomic clone 2370L14, DNA		
ACCESSION	sequence.		
VERSION	A0111002		
KEYWORDS	A0111002.1	GI:3487692	
SOURCE	GSS. human.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 443)	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building	Map Building (1998)	Unpublished Other-GSSs: CIT-HSP-2370L14.TF

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mda@amsl.tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M3 Reverse
Class: BAC ends.

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FEATURES
source
    location/Qualifiers
    1. .443
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="2370L14"
    /clone_11b="CIT-HSP"
    /sex="Male"
    /cell_type="Sperm"
    /note="Vector: pReloBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT
    120 a      127 c      82 g      114 t
ORIGIN

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Query Match	3 8%	Score 408.4;	DB 12;	Length 443;
Best Local Similarity	99.5%;	Pred. No. 9.3e-48;		
Matches 420;	Conservative	0;	Mismatches 1;	Indels 1;
Gaps 1;				
OY	2752	TGAGGGTATGCTTGTAGCCCAAGAAATTGAGCTGCGCATGAGCCATGATGTGCCACTG	2811	

[illegible]

RESULT	14
AA569989/c	
LOCUS	
DEFINITION	-453 bp mRNA linear EST 09-SEP-1997
ACCSSION	m47411.s1 NCI-CGAP-B _r 2 Homo sapiens CDNA clone IMAGE:1071428 3'',
VERSION	AA569989
KEYWORDS	AA569989.1 GI:2343969 EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (pages 1 to 453)	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap		
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			Unpublished (1997)	
Contact: Robert Strausberg, Ph.D.				
Email: cgapbs_r@mail.nih.gov				
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.				
CDNA Library Preparation: M. Bento Soares, Ph.D.				

```

FEATURES
Source
    1..453
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    CDNA Library Arrayed by: Greg Lennon, Ph.D.
    DNA Sequencing by: Washington University Genome
    Clone distribution: NCI-CCGAR clone distribution information can be
    found through the I.M.A.G.E. Consortium/LUNL at:
    www-bio.1nl.gov/bdip/image/image.html
    Insert length: 850 Std Error: 0.00
    Seq primer: -40ml3 fwd. RT from Amersham
    High quality sequence stop: 428.
    Location/Qualifiers

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/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -

```

[illegible]

OY	3165	ACAAGCTT	3172
Dd	54	ACATGCTT	47
RESULT	12		
LOCUS	AM299376/c		
DEFINITION	x839b06.x1 NCI.GCAP.Kid1l Homo sapiens cDNA clone IMAGE:2771987 3'	525 bp	mRNA linear EST 18-JAN-2000
ACCESSION	AM299376		
VERSION	AM299376		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	similar to contains element MER3J repetitive element ; , mRNA sequence.		
JOURNAL	NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: gcgaps-remail.nih.gov		
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, W.D., Ph.D.		
	cDNA Library Preparation: M. Bento Soares, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-GCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:		
	www.bio.llnl.gov/bdbp/image/image.html		
	Seq primer: -400P from Glibco		
	High quality sequence stop: 464.		
FEATURES	location/Qualifiers		
source	1..525		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone_image="IMAGE:2771987"		
	/clone_idb="NCI_GCAP_Kid11"		
	/lab_host="IDHI0B"		
	/note="Organ: kidney; Vector: pTZ19D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_GCAP_Kid3 was prepared, and ss circles were made in vitro. Following HspAmpification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cdnas from a pool of 5,000 clones made from the same library (clonesids 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."		
BASE COUNT	153 a 123 c 125 g 124 t		
ORIGIN			
Query Match	3.8%; Score 411.8; DB 9; Length 525;		
Best Local Similarity	99.1%; Pred. No. 2.9e-48;		
Matches 435; Conservative	0; Mismatches 2; Indels 2; Gaps 2;		
OY	8667	CGATCCACAGTCGATGCATTGTCTTTAAATGCCCTGAAGAAGTCTCGAATGTGAC	8726
Dd	525	CGATCCACAGTCGATGCATGTCTTTAAAGTCCCTGAAGAAGTCTCGAATGTGAC	466
OY	8727	TCCCTTGCTCCTCTGTGGCATTTCTTTGGACCTTAAGCAAGACTG	8786
Dd	465	TCCCTTGCTCCTCTGTGGCATTTCTTTGGACCTTAAGCAAGACTG	406
OY	8787	TAAATGGTGGGACAGCTAGTGGCCCTGTGGGCTTACACACGGTGTCCCTCCAGGCC	8846
Dd	405	TAAATGGTGGGACAGCTAGTGGCCCTGTGGGCTTACACACGGTGTCCCTCCAGGCC	346

|||||
Db 404 CCAGCCGCAAAAGAGCTTAATATATATCCAGATGCGATGCTTACTTATGCTTAC 345
Oy 9499 TACATGCACTGCTGCGCATTAATGCGTACAGCAATCTGCTGTAAGGCGAGTGCTTC 9468
Db 344 TACATGCACTGCTGCGCATTAATGCGTACAGCAATCTGCTGTAAGGCGAGTGCTTC 285
Oy 9469 AGATACCATTAACAGCTCAGAGCTTCTCTTAGCGCATTAATTTTACCAAGATATC 9528
Db 284 AGATACCATTAACAGCTCAGAGCTTCTCTTAGCGCATTAATTTTACCAAGATATC 225
Oy 9529 TCATCTCTCTTTTAAACCAATTTCTTTTGTGCTAGAAAAGTTATGTAAGAAAAG 9568
Db 224 TCATCTCTCTTTTAAACCAATTTCTTTTGTGCTAGAAAAGTTATGTAAGAAAAG 165
Oy 9569 TAAATGATTTAGCGCATTTGTAGAAAAGCTATAAATGATACAAATTAAGCTGTAT 9648
Db 164 TAAATGATTTAGCGCATTTGTAGAAAAGCTATAAATGATACAAATTAAGCTGTAT 105
Oy 9649 TTAATTAACCAAGTGAACCACTTGTCTATTACCTGTAGTATTGTTGC 9708
Db 104 TTAATTAACCAAGTGAACCACTTGTCTATTACCTGTAGTATTGTTGC -C 46
Oy 9709 ATTAAAAATGCATATCTTTTAATAAATGATATTGTTATA 9752
Db 45 ATTAAAAATGCATATCTTTTAATAAATGATATTGTTATA 2

RESULT 10
AM449998/c 442 bp mRNA linear EST 17-FEB-2000
LOCUS UI-H-B13-akv-c-07-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone
DEFINITION IMAGE:2735605 3', mRNA sequence.
ACCESSION AM449998
VERSION AM449998.1 GI:6990774
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 442)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/ILINr at:
www-bio.liln.gov/bdrip/image/image.html
Seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers

1..442

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2735605"

/lab_host="NCI_CGAP_Sub5"

/note="Vector: pT73D-Pac (Pharmacia)"

polylinker: Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5

is a subtracted library derived from NCI_CGAP_Sub4. The

single-stranded DNA preparation of NCI_CGAP_Sub4 was used

as a tracer in a subtractive hybridization with a driver

comprising: the IMAGE pool (NCI_CGAP_kids pool 1 LHAM

3334-3337, 3682-3683, 3798-3803 (IMAGE Clonoids

1322376-1323911, 1456008-1456775, 1500552-1502855);

NCI_CGAP_kids pool 1 LHAM 3338-3342, 3722-3725, 3776-3778

(IMAGE Clonoids 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lus pool 1 LHAM 3575-3582,
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520804-1522439
); NCI_CGAP_Gc4 pool 1 LHAM 3164-3167, 3716-3720,
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI_CGAP_Pr22 pool 1 LHAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clonoids 985608-986759
), 1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LHAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255
), 1144584-1145351). (10% of the driver population), plus a
pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE
Clonoids 2708616-2710535) and NCI_CGAP_Sub2 (IMAGE
Clonoids 2710536-2712455) (10% of the driver population
) , plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE
Clonoids 2712456-2723591) (10% of the driver population),
plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE
Clonoids 2723592-2728969) (70% of the driver population).
Subtraction was performed as previously described (Bonaldi
, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
Research 6, 791-806.
TAG_LIB=NCI_CGAP_Co10
TAG_TISSUE=Colon
TAG_SEO=AAACG"

BASE COUNT 93 a 125 c 134 g 90 t
ORIGIN

Query Match 3.9%; Score 420.8; DB 9; Length 442;
Best Local Similarity 99.5%; Pred. No. 1.7e-49;
Matches 422; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 325 GAAATTTAAGGGGAGCGGCGGCAAGCTGGGGAATGAGCCCGGAGCCAGCGCGG 384
Db 440 GGAATTTAAGGGGAGCGGCGGCAAGCTGGGGAATGAGCCCGGAGCCAGCGCGG 381
Oy 385 CTTCCTCCTCGATGCTTTTGCAGACCGGCGCTCAGGGGCGCTTGCCTGATGCC 444
Db 380 CTTCCTCCTCGATGCTTTTGCAGACCGGCGCTCAGGGGCGCTTGCCTGATGCC 321
Oy 445 GAGGCGTGGGCGGCAACTGAGGGGCGGGGCTGGAATAATCGAACTAGCTTTTCT 504
Db 320 GAGGCGTGGGCGGCAACTGAGGGGCGGGGCTGGAATAATCGAACTAGCTTTTCT 261
Oy 505 TTGCGCTGGGAGTTTGCTAACTTTGGAGGACCTGCTCAACCTATCCGCAAGCCCTCT 564
Db 260 TTGCGCTGGGAGTTTGCTAACTTTGGAGGACCTGCTCAACCTATCCGCAAGCCCTCT 201
Oy 565 CCTACTTCTGCTGCAGACCCGCTGAGGAGTGCCTACACTGAACTGAGATAGGG 624
Db 200 CCTACTTCTGCTGCAGACCCGCTGAGGAGTGCCTACACTGAACTGAGATAGGG 141
Oy 625 TCCTGCGCCGAGACCTGCCCCCTCCCGGCTGTCGCCGCTTGGGAGTGACTTTTG 684
Db 140 TCCTGCGCCGAGACCTGCCCCCTCCCGGCTGTCGCCGCTTGGGAGTGACTTTTG 81
Oy 685 GAACCGCCACCTCCCTCCGCCCACTAGATGCTTTAATAAATGCTAGTCTCTCAC 744
Db 80 GAACCGCCACCTCCCTCCGCCCACTAGATGCTTTAATAAATGCTAGTCTCTCAC 21
Oy 745 TTGA 748
Db 20 TTGA 17

RESULT 11
LOCUS A0790990/c 533 bp DNA linear GSS 03-AUG-1999
DEFINITION HS-2239.B1.D04.MR CTR Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate-2239 Col-7 Row-H, DNA sequence.
ACCESSION A0790990
VERSION A0790990.1 GI:5698614
KEYWORDS GSS.

REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.litlil.gov/bdrp/image/image.html Seq primer: -400P from GIDCO High quality sequence stop: 406. location/Qualifiers
FEATURES	source
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	/db.xref="taxon:9606"
	/clone="IMAGE:2470305"
	/clone_lib="NCI-CGAP_Kid12"
	/tissue_type="2 pooled tumors (clear cell type)"
	/lab_host="DH10B"
	/note="Organ: Kidney; Vector: pTR73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI-CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	171 a 84 c 82 g 183 t
ORIGIN	
Query Match	3.9%; Score 423.4; DB 9; Length 520;
Best Local Similarity	97.5%; Pred. Mis.6-9e-50;
Matches 430; Conservative	0; No.matches 11; Indels 0; Gaps 0.
OY	9312 CCCAAGTCGTAGATTACAGGTGATGGCACCCTCCGCCGCCTCAAGAAGTTTAAT 9371
DB	463 CCAGGCTCTGAGATTGAGAGGTGATGACCATCCCTCCAGCGCTCAAAAGACTTAAT 404
OY	9372 ATATATATCCAGATGGCATGTGTTTACTTATCTTACTACATGCACTTGCGCATTAAT 9431
DB	403 AATAATATCCAGATGGCATGTGTTTACTTATCTTACTACATGCACTTGCGCATTAAT 344
OY	9432 GTGGTCAAGCATTCGTGCTGTGAAGGCGAGTCTCAGGATACCATATACAGCTAGAA 9491
DB	343 GTGGTCAAGCATTCGTGCTGTGAAGGCGAGTCTCAGGATACCATATACAGCTAGAA 284
OY	9492 GTTTCCTCTTAGGCATTAATTATAGCAAAGATATCTCATCTCTCTTTAAACATT 9551
DB	283 GTTTCCTCTTAGGCATTAATTATAGCAAAGATATCTCATCTCTCTTTAAACATT 224
OY	9552 TCCTTTTTTGTGTGAAGAAAGTTAGTAGAAAAAGTAATGTGAATTACGGCTCATGT 9611
DB	223 TCCTTTTTTGTGTGAAGAAAGTTAGTAGAAAAAGTAATGTGAATTACGGCTCATGT 164
OY	9612 AGAAAAGCTATPAANAATGATATACATTTAAGCTGTATTTAATTAGCAGTGAANAATAT 9671
DB	163 AGAAAAGCTATPAANAATGATATACATTTAAGCTGTATTTAATTAGCAGTGAANAATAT 104
OY	9672 TAACAATCTGCATTCACCGCTTAGTATTAATGTGGCATTAATAAATGCATATACCTTAAT 9731
DB	103 TAACAATCTGCATTCACCGCTTAGTATTAATGTGGCATTAACAATGCATATACCTTAAT 44

	DB	9732	AAATGTAATGTAGTATA 9752 N93736/c
	Db	43	AAATGTCACAAAATTGTAA 23
	RESULT	9	N93736 520 bp RNA linear EST 20-AUG-1996
	LOCUS		ZB5J806.sI Soares fetal_lung.NbHt19w Homo sapiens cDNA clone
	DEFINITION		IMAGE:307162 3' similar to gb:M5505 CTOCHROME P450 IAZ (HUMAN);,
	ACCESSION		mRNA sequence.
	VERSION		N93736
	KEYWORDS		N93736.1 GI:1266045
	SOURCE		EST.
	ORGANISM		human.
	REFERENCE		Homo sapiens
	AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 520) Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiappelli,B., Chissoe,S., Dietrich,N., Dubuca,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore, 'M.', Mullins,M., Kucaba,J., Prange,C., Rifkin,L., Rohlfing,T., 'B.', Morris,M., Parsons,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaslis,E., Schellenberg,K., Soares,K.P., Waterston,R., Wilson,R. and Warrar,M. Underwood,K., Wohlmann,P., Westerton,R., Wilson,R. and Marras,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
	TITLE		Genome Res. 6 (9), 807-828 (1996)
	JOURNAL		97044478
	MEDLINE		Contact: Wilson RK
	COMMENT		Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1642 Std Error: 0.00 Seq primer: mob.RCGA+ET High quality sequence stop: 328. Location/Qualifiers 1..520 /organism="Homo sapiens" /db_xref="GBD:1250574" /db_xref="Taxon:9606" /clone="IMAGE:307162" /clone_1lb="Soares,fetal_lung_NbHt19w" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /note="Organ: lung; Vector: pRT73D (Pharmacia) with a modified polylinker, site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTGCACAATCTGAAGTAGGGAGCCGCCCAATTTTTTTTTTTTTTTT-3']; double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bernaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHt19w."
	FEATURES		
	Source		
	BASE COUNT		175 a 94 c 88 g 161 t 2 others
	ORIGIN		
	Query Match		3.9%, Score 421.6; DB 10; Length 520;
	Best Local Similarity		98.5%; Pred. No. 1.2e-49;
	Matches 457; Conservative		0; Mismatches 4; Indels 3; Gaps 1
	Dn	464	GTCGACGCGCTGCCTGGNCSTCCCAAAGTCTAGATTACCAGGTGTAGCCACACTGC 405
	OY	9349	CAGCAGCGTAAAAAGAGTCTTAATATATATATCATCAGATGCATGTGTTTACTTTATGTGTAC 9408

prepared, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo.

BASE COUNT 153 a 77 c 68 g 141 t 1 others
ORIGIN

Query Match 4.0%; Score 429.4; DB 9; Length 440;
Best Local Similarity 98.4%; Pred. No. 1.1e-50;
Matches 433; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 9313 CCAAGTGTGAGATTCAGTGTGAGCCACCCGCGCAAGAGAGTCTTAATA 9372
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 440 CCAGGTCCTGAGATGAGGTGTGAGCCACCCGCGCAAGAGAGTCTTAATA 381
QY 9373 TATATCCAGATGGCATGTGTACTTTATGTTACTACATGCACCTGGCCGATTAATG 9432
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 380 TATATATCCAGATGGCATGTGTACTTTATGTTACTACATGCACCTGGCCGATTAATG 321
QY 9433 TGGTCAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACATCAGAAG 9492
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 320 TGGTCAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACATCAGAAG 261
QY 9493 TTTCTCTTGTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTT 9552
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 260 TTTCTCTTGTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTT 201
QY 9553 CTTTCTTGTAGGATTAAGAAATATATGAGAAAGAAATGATTTACGCTCATTTGA 9612
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 200 CTTTCTTGTAGGATTAAGAAATATATGAGAAAGAAATGATTTACGCTCATTTGA 141
QY 9613 GAAAGCTATTAATGAATACATTAAGCTGTATTTAATAGCCAGGAAACATTT 9672
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 140 GAAAGCTATTAATGAATACATTAAGCTGTATTTAATAGCCAGGAAACATTT 81
QY 9673 AACACTGTCTATTTACCTGTATTTATTTGTCATTAATAATCATATCTTTAATA 9732
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 80 AACACTGTCTATTTACCTGTATTTATTTGTCATTAATAATCATATCTTTAATA 21
QY 9733 AATGTATTTGTATTGATA 9752
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 20 AATGTATTTGTATTGATA 1

RESULT 7
AAB76054/c 439 bp mRNA linear EST 31-MAR-1998
LOCUS nrl4d03.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:116197 3'
DEFINITION similar to contains element MER36 repetitive element ; mRNA
sequence.

ACCESSION AAB76054
VERSION AAB76054.1 GI:2984817
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 439)
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-rt@mail.nih.gov
Tissue Procurement: Ilian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Insert Length: 865 Std Error: 0.00
Seq primer: -40m13 fwd, 5' from Amersham
High quality sequence stop: 421.
location/Qualifiers

FEATURES
source 1. .439
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1161797"
/clone_lib="NCI_CGAP_Co10"
/tissue_type="colon tumor RER+"
/lab_host="DH10B"

/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dN) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4)."

BASE COUNT 154 a 77 c 66 g 142 t
ORIGIN

Query Match 3.9%; Score 427; DB 9; Length 439;
Best Local Similarity 98.9%; Pred. No. 2.3e-50;
Matches 430; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9318 GTGCTGAGATTCACAGTGTGAGCCACCCGCGCAAGAGAGTCTTAATATAT 9377
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 439 GTGCTGAGATTCACAGTGTGAGCCACCCGCGCAAGAGAGTCTTAATATAT 380
QY 9378 ATCCAGATGGCATGTGTACTTTATGTTACTACATGCACCTGGCGCATTAATG 9437
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 379 ATCCAGATGGCATGTGTACTTTATGTTACTACATGCACCTGGCGCATTAATG 320
QY 9438 CAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACATCAGAAGTTTCT 9497
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 319 CAAGCATTCCTGCTTGAAGGAGGCTGCTCAGATACATATACATCAGAAGTTTCT 260
QY 9498 TCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTTCTTT 9557
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 259 TCTTTAGCATTAATTTTACGAAGATATCTCATCTCTTTTAAACATTTTCTTT 200
QY 9558 TTTGTGTTAGAAAGTTATGTAGAAAAAGTAATGTGATTTACGCTCATTTGAGAAA 9617
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 199 TTTGTGTTAGAAAGTTATGTAGAAAAAGTAATGTGATTTACGCTCATTTGAGAAA 140
QY 9618 GCTATTAATGAATACATTAAGCTGTATTTAATTTAGCCAGTGAAGAACTTTAACA 9677
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 139 GCTATTAATGAATACATTAAGCTGTATTTAATTTAGCCAGTGAAGAACTTTAACA 80
QY 9678 CTGTCTATTTACCTGTATTTATTTGTTGCATTAATAATCATATCTTTAATAATGT 9737
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 79 CTGTCTATTTACCTGTATTTATTTGTTGCATTAATAATCATATCTTTAATAATGT 20
QY 9738 AATTTGTATTGATA 9752
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 19 AATTTGTATTGATA 5

RESULT 8
A1949947 520 bp mRNA linear EST 06-SEP-1999
LOCUS wq04f05.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2470305 3'
DEFINITION mRNA sequence.

ACCESSION A1949947
VERSION A1949947.1 GI:5742257
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

QY 4588 GGAGTTTCAGAGTGGCTGAGGCTGTGCTCCCAATTCGGGAAGGACTTTCTCA 4647
 |||||||
 Db 282 GGAGTTTCAGAGTGGCTGAGGCTGTGCTCCCAATTCGGGAAGGACTTTCTCA 341
 QY 4648 ATCTAGAGTCTCTACCTTAATTAATGAGATGTATGAGACGCCACAAGTCATGGTTTAA 4707
 |||||||
 Db 342 ATCTAGAGTCTCTACCTTAATTAATGAGATGTATGAGACGCCACAAGTCATGGTTTAA 401
 QY 4708 TTTCTTTTTCATGATATGGCTCAAGGAGTGTCTATGAGCCCTGCTTTTATTTA 4767
 |||||||
 Db 402 TTTCTTTTTCATGATATGGCTCAAGGAGTGTCTATGAGCCCTGCTTTTATTTA 461
 QY 4768 ACCAATAATCTTTTATATTTATTTATCTGTTAAAAATTCAGAAATTCAGAGCCGGGAC 4827
 |||||||
 Db 462 ACCAATAATCTTTTATATTTATTTATCTGTTAAAAATTCAGAAATTCAGAGCCGGGAC 521
 QY 4828 GGTGGCTCA 4836
 |||||||
 Db 522 GGTGGCTCA 530

RESULT 5
 A1127651 438 bp mRNA linear EST 27-OCT-1998
 LOCUS uc30h07.x1 Soares_pregnant_uterus_NbHpu Homo sapiens cDNA clone
 DEFINITION IMAGE:1711165.3 similar to contains element MER36 repetitive
 element ;, mRNA sequence.

ACCESSION A1127651
 VERSION A1127651
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 438)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 669 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 415.
 Location/Qualifiers
 1. 438
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1711165"
 /clone_lib="Soares_pregnant_uterus_NbHpu"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: uterus; Vector: pTV3-Pac; Site_1: Not I;
 Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
 oligo(dT) primer [5',
 AACTGAGAAATTCGGCGCCCTTTTCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pTV3 vector. Library
 went through one round of normalization. Library
 constructed by M. Fatima Bonaldo."

BASE COUNT 153 a 73 c 67 g 145 t
 ORIGIN

Query Match 4.0%; Score 429.6; DB 9; Length 438;
 Best Local Similarity 99.1%; Pred. No. 1e-50;
 Matches 432; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9317 AGTGTGAGATTACAGGTGTGAGCCACCCTGGCCGCGTCAAAAGAGTCTTAATATA 9376
 |||||||
 Db 438 AGTGTGAGATTACAGGTGTGAGCCACCCTGGCCGCGTCAAAAGAGTCTTAATATA 379
 QY 9377 TATCCAGATGGCATGTGTTTACTTTATGTATGTTACATGCACTTGGCTGATTAATGTGCT 9436
 |||||||
 Db 378 TATCCAGATGGCATGTGTTTACTTTATGTATGTTACATGCACTTGGCTGATTAATGTGCT 319
 QY 9437 ACAAGCATCTGTCTTGAAGGGCAGAGTGTCTGAGATACATATACAGCTCAGAGTTTC 9496
 |||||||
 Db 318 ACAAGCATCTGTCTTGAAGGGCAGAGTGTCTGAGATACATATACAGCTCAGAGTTTC 259
 QY 9497 TTTCTTAGCATTAATATTTAGCAAGATATCTCAGCTCTTTTAAACCATTTTCTTT 9556
 |||||||
 Db 258 TTTCTTAGCATTAATATTTAGCAAGATATCTCAGCTCTTTTAAACCATTTTCTTT 199
 QY 9557 TTTTGTGTAGAAAAGTTATGTAGAAAATAATGATTTACGTCATTTAGAAA 9616
 |||||||
 Db 198 TTTTGTGTAGAAAAGTTATGTAGAAAATAATGATTTACGTCATTTAGAAA 139
 QY 9617 AGCTATAAATGAAATCAATTAAGCTTTATTAATTAGCCAGTGAATAAATTAACA 9676
 |||||||
 Db 138 AGCTATAAATGAAATCAATTAAGCTTTATTAATTAGCCAGTGAATAAATTAACA 79
 QY 9677 ACTGTCTATTACCTGTAGTATTTATTTGCTTAAATGATATCTTAATAATG 9736
 |||||||
 Db 78 ACTGTCTATTACCTGTAGTATTTATTTGCTTAAATGATATCTTAATAATG 19
 QY 9737 TATATTTGATTGTATA 9752
 |||||||
 Db 18 TATATTTGATTGTATA 3

RESULT 6
 A0469921/c 440 bp mRNA linear EST 24-FEB-2000
 LOCUS ha27e08.x1 NCI-CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2674950.3
 DEFINITION similar to contains Alu repetitive element;., mRNA sequence.

ACCESSION A0469921
 VERSION A0469921
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 440)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmer-Buck, M.D., Ph.D.
 cDNA Library preparation: M. Bento Soares, Ph.D.
 DNA library Arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 www-bio.lnl.gov/bbrp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 439.
 Location/Qualifiers
 1. 440
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2674950"
 /clone_lib="NCI-CGAP_Kid12"
 /tissue_type="2 pooled tumors (clear cell type)"
 /lab_host="DH10B"
 /note="Organ: Kidney; Vector: pTV3D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Plasmid DNA from the normalized library NCI-CGAP_Kids was

DEFINITION	EST186265 MAGE resequences, MAGM Homo sapiens CDNA, mRNA sequence
ACCESSION	AM974162
VERSION	AM974162.1 GI:8165353
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 545) Hedge, P., Qi, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J. and Quackenbush, J.
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
JOURNAL	Unpublished (2000)
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johng@tigr.org Plate: 330
FEATURES	Seq. primer: Forward
source	Location/Qualifiers 1..545 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE resequences, MAGM" /note="Vector: pBluescriptSKm"
BASE COUNT	153 a 137 c 123 g 132 t
ORIGIN	
Query Match	4.3%; Score 464.8; DB 9; Length 545;
Best Local Similarity	93.8%; Pred. No. 1,1e-55;
Matches 484; Conservative	0; Mismatches 32; Indels 0; Gaps 0;
QY 8576	GAAAGAGAGAGATGGCTCTCTGTGTGCATGTGTCTTCTTCTGACGAGCTTGAAT 8635
DB 544	GAAAGGGGGGTGGCTTCTTTTCTTGTCTCCAAAGGGTTTCTTTAAGGAGCTTGAAT 485
QY 8636	CACATGAAAGGGGAAACAGAAACAAACCACTGATCTCTAGCTGTGATGTTTCTTTAA 8695
DB 484	CCCAAGAAAGGGGACACAGAAACAAACCACTGTTCCAAAGGGGTATGTTCTTTTAA 425
QY 8696	AAATCCCTGAAGAGAGTCTCTGGAATGTGACTCCCTTGCCTCTGTGTCTCTTTTGGC 8755
DB 424	AAATCCCTGAAGAGAGTCTCTGGAATGTGACTCCCTTGCCTCTGTGTCTCTTTTGGC 365
QY 8756	ATTTCATTTTCTTGGACCTTACGACGAAGAGCTGTAATTTGGTGGGACAGCTAGTGCCCTCG 8815
DB 364	ATTTCATTTTCTTGGACCTTACGACGAAGAGCTGTAATTTGGTGGGACAGCTAGTGCCCTCG 305
QY 8816	TGGGCTTTCACACAGCGTGTCTCTCTTAAGCCAGTGTCTGTGAGTCAAGACTCTGGTGT 8875
DB 304	TGGGCTTTCACACAGCGTGTCTCTCTTAAGCCAGTGTCTGTGAGTCAAGACTCTGGTGT 245
QY 8876	ATTTCCTCATTAAGTAGAGTAAGCTGTGCATTTTGAATGATATTAATGAAGACACC 8935
DB 244	ATTTCCTCATTAAGTAGAGTAAGCTGTGCATTTTGAATGATATTAATGAAGACACC 185
QY 8936	AAATGGCTTAAGAGATGCCAGAGTCTCTTCATGAGGACACATGGGGTTCCGGTGCACATTA 8995
DB 184	AAATGGCTTAAGAGATGCCAGAGTCTCTTCATGAGGACACATGGGGTTCCGGTGCACATTA 125
QY 8996	AAAAAAAATCTTACCCAGGACATTTAGGAATTTGTAGATTTCTGGGAATCAGTTTCAACAT 9055
DB 124	AAAAAAAATCTTACCCAGGACATTTAGGAATTTGTAGATTTCTGGGAATCAGTTTCAACAT 65
QY 9056	GTTCAAAAGAGCTTTTTTTTTTTTTTTTGTAGACTCA 9091
DB 64	GTTCAAAAGAGCTTTTTTTTTTTTTTTTGTAGACTCA 29

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
4	A0703007	Homo sapiens genomic clone Plate-1019 Col-17 Row-N, DNA sequence.	AF0703007	GI:5412433	GSS.	human.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	531 bp DNA linear GSS 07-Jul-1999	
TITLE	JOURNAL	MEDLINE	COMMENT						
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)	99380589	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu						
Clones are derived from the human BAC library RPCL11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (http://inforesgen.com). BAC end Web Server: http://www.husc.washington.edu									
Seq primer: 17									
Class: BAC ends									
Location/Qualifiers									
1..531									
/organism="Homo sapiens"									
/db_xref="taxon:9606"									
/clone="Plate-1019 Col-17 Row=N"									
/clone_11b="RPCL11 Human Male BAC Library"									
/sex="male"									
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and PbaCI methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"									
BASE COUNT	129 a	114 c	146 g	137 t	5 others				
ORIGIN									
Query Match	4.3%	Score 464.2;	DB 12;	Length 531;					
Best local Similarity	96.5%;	Pred. No. 1.3e-55;							
Matches 472;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;					
OY 4348	ACACTGGATTGGAGGACACAGAACCCAGGGCGTGGGCCCAAGCGGGAGTGGAAGC	4407							
Dd 42	ACACTGGATTGGAGGACACAGAACCCAGGGCGTGGGCCCAAGCGGGAGTGGAAGC	101							
OY 4408	CACAAATTCGGGCCCAGGCAGAACAAGGCTTAACCTGTGAAGAGGACCTCCCTGCACAGCTG	4467							
Dd 102	CTCTGTGATTCGGGCCCCAGGCAGAACAAGGCTTAACCTGTGAAGAGGACCTCCCTGCACAGCTG	161							
OY 4468	CAGAGTGTGTTGAGAGTGGAGAGAGTGTGTTGGACCACAAAGATATGGTGAACACAC	4527							
Dd 162	CAGAGTGTGTTGAGAGTGGAGAGAGTGTGTTGGACCACAAAGATATGGTGAACACAC	221							
OY 4528	TTCGCCCCCTAATCTCTAGTGCAGAGTGGAGAGAGTGTGTCAGGGCACAGAAATCCCTGGTT	4587							
Dd 222	TTCGCCCCCTAATCTCTAGTGCAGAGTGGAGAGAGTGTGTCAGGGCACAGAAATCCCTGGTT	281							

Query Match 5.7%; Score 612.8; DB 10; Length 691;
 Best Local Similarity 98.9%; Pred. No. 1.9e-76;
 Matches 617; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1397 TACAGCTGCTTCTAATCTAGTTGACAGATGATTTGCCCTAGTGTAGACACAGTGTCT 1456
 |||||||
 DB 691 TACAGCTGCTTCTAATCTAGTTGACAGATGATTTGCCCTAGTGTAGACACAGTGTCT 632
 QY 1457 GTGGGTACACGCGCGGCTCAGACAGCACTTGAGTTTGTACTAGCTATGATCTTAACAT 1516
 |||||||
 DB 631 GTGGGTACACGCGGCGCTCAGACAGCACTTGAGTTTGTACTAGCTATGATCTTAACAT 572
 QY 1517 TTTACACATGACAGATGAGGACATGCGAGCGCTGCTTCTCGCAATTTATTCATG 1576
 |||||||
 DB 571 TTTACACATGACAGATGAGGACATGCGAGCGCTGCTTCTCGCAATTTATTCATG 512
 QY 1577 TACACGGGCTTTGGTGAGAGCTCATGTCTCCACTTCATAGCTATGATCTTAACAT 1636
 |||||||
 DB 511 TACACGGGCTTTGGTGAGAGCTCATGTCTCCACTTCATAGCTATGATCTTAACAT 452
 QY 1637 CACACTGCATTTAGAGGTGATTAATAATTTTCATGTTGAGCAGAAATTTCAATGTTTA 1696
 |||||||
 DB 451 CACACTGCATTTAGAGGTGATTAATAATTTTCATGTTGAGCAGAAATTTCAATGTTTA 392
 QY 1697 CAAGTGAATGATGATGCGGAGCATGATGTTGACCTGTTCAAGGCCCAAGGAGAGAGAG 1756
 |||||||
 DB 391 CAAGTGAATGATGATGCGGAGCATGATGTTGACCTGTTCAAGGCCCAAGGAGAGAGAG 332
 QY 1757 GAAACAAGCTTTTACCCTTTGATTTTTCATTTGATTTGATTTGAGGAGAGATGACATAAGCAA 1816
 |||||||
 DB 331 GAAACAAGCTTTTACCCTTTGATTTTTCATTTGATTTGAGGAGAGATGACATAAGCAA 272
 QY 1817 TGACGAGAAGATATATCAATCATCAGAAATCATGAGTGTGTTGAGAGACAGAGAGTAC 1876
 |||||||
 DB 271 TGACGAGAAGATATATCAATCATCAGAAATCATGAGTGTGTTGAGAGACAGAGAGTAC 212
 QY 1877 GGCAGATCACTCTGGGCTGACACTTGAGCAGACATGAAAGAAATTAAGATGATATG 1936
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 DB 211 GGCAGATCACTCTGGGCTGACACTTGAGCAGACATGAAAGAAATTAAGATGATATG 152
 QY 1937 ACTGGGAGAGATTTTCCAGGCAAACTGATGGGCTGGGCAAGTTGATTAATAAGCGG 1996
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 DB 151 ACTGGGAGAGATTTTCCAGGCAAACTGATGGGCTGGGCAAGTTGATTAATAAGCGG 92
 QY 1997 GTTTTCTCAGCACTACTCATGTGT 2020
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 DB 91 GTTTTCTCAGCGGCGCGCTGGGT 68

RESULT 2
 AG116246/c 648 bp DNA linear GSS 03-NOV-2001
 LOCUS AG116246
 DEFINITION Pan troglodytes DNA, clone: PTB-123L15.R, genomic survey sequence.
 AG116246
 VERSION AG116246.1 GI:16736765
 KEYWORDS GSS: GSS (genome survey sequence);
 SOURCE Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
 BAC library clone:PTB-123L15.R.

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 REFERENCE
 1 (sites)
 Fujiiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of library PTB
 JOURNAL Unpublished
 2 (bases 1 to 648)
 REFERENCE
 Fujiiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-2001) Asao Fujiiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbasesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.

PRIMERS

Sequencing: MJ3Rev

LIBRARY

Vector : pRS145

R.site 1 : SacI

R.site 2 : SacI.

FEATURES

source

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 /db_xref="taxon:9598"
 /clone="PTB-123L15.R"
 /sex="male"
 /cell_type="lymphoblast"

/clone_11b="PTB Chimpanzee Male BAC Library"

BASE COUNT

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ORIGIN

Query Match 5.4%; Score 589; DB 12; Length 648;
 Best Local Similarity 99.2%; Pred. No. 4.2e-73;
 Matches 592; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1006 GAGAGTCTCTAGGAGGAGGCTCCTGAGAGAGGCTACCTCGGCGCTTCCCACTCTT 1065
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 DB 648 GAGAGTCTCTAGGAGGAGGCTCCTGAGAGAGGCTACCTCGGCGCTTCCCACTCTT 589
 QY 1066 GGCATTTGTTCTTTGCGCGGAAATTAAGTATATGATGATTTTGAACGTTTGAACGAA 1125
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 DB 588 GGCATTTGTTCTTTGCGCGGAAATTAAGTATATGATGATTTTGAACGTTTGAACGAA 529
 QY 1126 CAATTCCTTTTGGCTAGGCTTTATGATTTGCAATGCTGTGTATTAAGAGCCTC 1185
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 DB 528 CAATTCCTTTTGGCTAGGCTTTATGATTTGCAATGCTGTGTATTAAGAGCCTC 469
 QY 1186 TCTACAAATGATGATTAATGACATGTAAGCAATGCACTCACTCTTAAGTTACATTCATA 1245
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 DB 468 TCTACAAATGATGATTAATGACATGTAAGCAATGCACTCACTCTTAAGTTACATTCATA 409
 QY 1246 TCTGATCTTATTTGATTTTCACTAGGCAATGAGGAGTAGAGCTTAATTAATTCGTTTATT 1305
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 DB 408 TCTGATCTTATTTGATTTTCACTAGGCAATGAGGAGTAGAGCTTAATTAATTCGTTTATT 349
 QY 1306 TACTAGACGTTTACGGAATTCAGATTTATTAATCTTTTACAGGTTTCAAAAGAACATATA 1365
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 DB 348 TACTAGACGTTTACGGAATTCAGATTTATTAATCTTTTACAGGTTTCAAAAGAACATATA 289
 QY 1366 TAATCTGGTTTCTCGATGTTTATTTCAAGTACTACAGCTGCTTCAATCTTATGTTACAGT 1425
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 QY 1546 CGGCGCTTCCCGGAAATTAATTCATGATGATGATGATGATGATGATGATGATGATGAT 1602
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 DB 108 CGGCGCTTCCCGGAAATTAATTCATGATGATGATGATGATGATGATGATGATGATGAT 52

RESULT 3
 AW974162/c 545 bp mRNA linear EST 02-JUN-2000
 LOCUS AW974162

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 13:30:58 ; Search time 7317.93 seconds

(without alignments)
19965.282 Million cell updates/sec

Title: US-09-497-957-1

Perfect score: 10825
Sequence: 1 TCTAAGCTTGAGATAAATTT.....TCCCCAAATTTTCATTAAC 10825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: qb_estl:*
10: qb_est2:*
11: qb_hlc:*
12: qb_gss:*
13: em_gss_hum:*
14: em_gss_hiv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	589	5.4	646	12	AG116246 Pan trogl
C 3	464.8	4.3	545	9	AW974162 EST86265
C 4	464.2	4.0	531	12	AQ703007 HS_5443_B
C 5	429.4	4.0	438	9	A1127651 qc3h07.x
C 6	429.4	4.0	440	9	AA69921 ha27e08.x
C 7	427	3.9	439	9	AA876054 nr14d03.s
C 8	423.4	3.9	439	9	AA876054 nr14d03.s
C 9	421.6	3.9	420	10	A1949947 wq04f05.x
C 10	420.8	3.9	442	9	N93736 2b51g06.s1
C 11	412.6	3.8	533	12	AW449998 UT-H-B13
C 12	411.8	3.8	525	9	AQ790990 HS_2239_B
C 13	408.4	3.8	443	12	AW299376 xs39b06.x
C 14	404.6	3.7	453	9	AQ111002 CTF-HSP-2
C 15	393.8	3.6	457	9	AA569989 nm47g11.s
C 16	387.4	3.5	392	9	AA160732 qb49b10.x
C 17	380.2	3.5	805	10	AA122894 OK31a01.s
					BG402460 602466163

C 18	375.2	3.5	380	9	A1040303
C 19	369.8	3.4	385	9	A1760080
C 20	363.8	3.4	454	9	A1358948
C 21	363.2	3.3	393	9	A1763178
C 22	360.2	3.3	448	9	A1368750
C 23	350.6	3.3	540	9	AA088873
C 24	350.6	3.2	441	10	R76697
C 25	342.2	3.2	388	10	BF445847
C 26	341.2	3.2	368	10	BF739151
C 27	324.2	3.0	334	9	AW902003
C 28	317.2	2.9	445	10	H01502
C 29	316.4	2.9	318	10	BF446089
C 30	313.4	2.9	326	12	AQ056874
C 31	293	2.7	420	12	AQ296898
C 32	285.2	2.6	392	10	BF405650
C 33	283	2.6	308	9	AA319758
C 34	280.2	2.6	822	10	BG249643
C 35	278	2.6	612	12	AQ395455
C 36	278	2.6	650	12	AG116352
C 37	277.4	2.6	6146	12	AQ839831
C 38	275.8	2.5	299	10	R07647
C 39	272.2	2.5	384	9	A1079088
C 40	272.2	2.5	456	12	AQ483293
C 41	271.8	2.5	339	9	AA102329
C 42	271.8	2.5	658	12	AG183592
C 43	271	2.5	759	12	AG185133
C 44	271	2.5	817	9	AL562711
C 45	270.6	2.5	444	12	B89781

ALIGNMENTS

RESULT 1	BG926549	691 bp	MRNA	linear	EST 06-NOV-2001
LOCUS	BG926549/c				
DEFINITION	HNC42-1-G8. R HNC (Human Normal Cartilage)			Homo sapiens	cDNA, mRNA
ACCESSION	BG926549				
VERSION	BG926549.1	GI:14321072			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo. 1 (bases 1 to 691)				
AUTHORS	Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathie,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.				
TITLE	Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries				
JOURNAL MEDLINE	osteoarthritis cartilage 9 (7), 641-653 (2001)				
COMMENT	Contact: Sanjay Kumar				

FEATURES

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	/tissue_type="cartilage"
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	/note="Vector: pSPORT II; Site_1: SalI; Site_2: NotI; Directional"
BASE COUNT	182 a 179 c 137 g 193 t
ORIGIN	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 13:57:28 ; Search time 174.74 Seconds
(without alignments)
15216.795 Million cell updates/sec

Title: US-09-497-957-1
Perfect score: 10825
Sequence: 1 TCTAAGTTGAGATAAAATT.....TCCCCAAATTTTCATAAAC 10825

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 363533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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6: /cgn2.6/ptodata/2/ina/backfiles.seq:*

363533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

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6: /cgn2.6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	10823	100.0	10825	3 US-08-652-265-3	Sequence 3, Appli
3	10823	100.0	10825	3 US-08-652-265-5	Sequence 5, Appli
4	10823	100.0	10825	3 US-08-652-265-7	Sequence 7, Appli
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7	10823	100.0	10825	3 US-08-834-497A-5	Sequence 5, Appli
8	10823	100.0	10825	3 US-08-834-497A-7	Sequence 7, Appli
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11	10823	100.0	10825	4 US-09-503-444A-5	Sequence 5, Appli
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13	10823	100.0	246240	2 US-08-724-394A-20	Sequence 20, Appl
14	10823	100.0	246240	2 US-08-724-394A-21	Sequence 21, Appl
15	10823	100.0	246240	2 US-08-724-394A-22	Sequence 22, Appl
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17	10511.6	9.7	2506	4 US-09-277-457-1	Sequence 1, Appli
18	516	4.8	517	1 US-08-632-673B-3	Sequence 3, Appli
19	516	4.8	517	1 US-08-632-673B-4	Sequence 4, Appli
20	516	4.8	517	1 US-08-632-673B-13	Sequence 13, Appl
21	516	4.8	517	3 US-08-652-265-20	Sequence 20, Appl
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23	516	4.8	517	3 US-08-834-497A-20	Sequence 20, Appl
24	516	4.8	517	3 US-08-834-497A-21	Sequence 21, Appl
25	516	4.8	517	4 US-09-503-444A-21	Sequence 20, Appl
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27	359	3.3	360	3 US-08-905-124-5	Sequence 5, Appli

28	355.8	3.3	14796	4	US-08-975-080-35	Sequence 35, Appl
29	355.8	3.3	14796	4	US-09-630-706-10	Sequence 10, Appl
30	355.8	3.3	14796	4	US-09-496-694B-3	Sequence 3, Appli
31	329.8	3.0	84495	4	US-09-797-906-3	Sequence 3, Appli
32	322.8	3.0	15977	4	US-08-608-285A-59	Sequence 59, Appl
33	320.8	3.0	7210	2	US-08-257-963B-10	Sequence 10, Appl
34	320.8	3.0	7210	4	US-08-367-841A-10	Sequence 10, Appl
35	320.8	3.0	7210	5	PCT-US95-07201-10	Sequence 10, Appl
36	320.8	3.0	22481	4	US-08-367-841A-43	Sequence 43, Appl
37	320.8	3.0	22481	5	PCT-US95-07201-43	Sequence 43, Appl
38	320.2	3.0	7210	2	US-08-257-963B-10	Sequence 10, Appl
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42	320.2	3.0	22481	5	PCT-US95-07201-43	Sequence 43, Appl
43	320	3.0	1440	3	US-08-652-265-9	Sequence 9, Appli
44	320	3.0	1440	3	US-08-652-265-10	Sequence 10, Appl
45	320	3.0	1440	3	US-08-652-265-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-652-265-1
Sequence 1, Application US/08652265
Patent No. 6025130
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: Join(361..436, 3762..4025, 4235..4510, 5606..5881,
6040..6153, 7107..7147)
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; (unaffected)"
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; NAME/KEY: allele
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; OTHER INFORMATION: /phenotype= "normal or wild-type
; (unaffected)"
; OTHER INFORMATION: /label= 24d1
; US-08-652-265-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 781 AACTCGGGTTTATTTCCCAATGTGAGTGTGAGTGTTCCTCCCGCACTCTCTCAACACAG 840
Qy 841 AAGTTCTTCCCTGAGTGTTCGCGAGAGAGGCTGAGCAAAACCCACAGAGGATCCGCAGG 900
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RESULT 2

US-08-652-265-3
; Sequence 3, Application US/08652265
; Patent No. 6025130

GENERAL INFORMATION:

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; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
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; INFORMATION FOR SEQ ID NO: 3:
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; US-08-652-265-3

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QY 7681 CATCTGATTTGATGTAGTTGACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
Db 7682 CATCTGATTTGATGTAGTTGACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
QY 7741 GCACCTGTCCCAAGAAAAGCATATGCTATCTGTGGGTAGTATGATGGTGTATTTAGC 7800
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QY 7861 AGGTGTCTACAGATTTTCAAGTTTAAATGGTGCCTTCATTTGGGATGCTACTAGTAT 7920
Db 7862 AGGTGTCTACAGATTTTCAAGTTTAAATGGTGCCTTCATTTGGGATGCTACTAGTAT 7920
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Db 7922 TCCAGACCTGAAGATCAACAATAATTTCTACCTGGTCTCTCCTTCTGTTCTGATAATGAA 7980

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QY 8041 CATGCATTAAGTGCATCTTCTTACATAATTTATGAGATAGGTACTTATTCCTCCAT 8100
Db 8042 CATGCATTAAGTGCATCTTCTTACATAATTTATGAGATAGGTACTTATTCCTCCAT 8100
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Db 8162 AGCAGCTTTGGGAGGCAAGCGGGTGGATCAGAGGTCAGAGATCGAGACCATCTGCG 8220
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QY 8881 CCTCAATGAAGTGGAGTAACT 8940
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QY 9001 AAAATTAACACAGGACTTCAGGAATTTAGATTTCTGGGAAATCAGTTCCACCATGTTCA 9060
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Db	10261	TTTTTCTGGCTTTATTATATAAATCTTTAAGGTCAACTACATTTTGAAAAATCAAGACCTG	10320
Qy	10321	CATTTTAAATCTTATTACACCTCTGGCAAAACCATTCACAAACCATGGTAGTAAAGAGAA	10380
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Db	10381	GGGTGACACCTGGTGGCCATAGGTAAATGTACACAGCTGGTCCGGTGACCAGAGATGCAG	10440
Qy	10441	CGCTGAGGGTTTTCTCTGAAGGTAAAGGAATTAAGAATGGGTGGAGGGGGTGTCACCTGGAA	10500
Db	10441	CGCTGAGGGTTTTCTCTGAAGGTAAAGGAATTAAGAATGGGTGGAGGGGGTGTCACCTGGAA	10500
Qy	10501	ATCACTTGTAGAGAAAAGCCCTGAAATTTTGAGAAAACAACAAGAACTACTTACCAG	10560
Db	10501	ATCACTTGTAGAGAAAAGCCCTGAAATTTTGAGAAAACAACAAGAACTACTTACCAG	10560
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Db	10681	TGAGAGGTACAGGCCAAAATCTTATGTTGTATTATAATATGTCATCTTTATAATACTCT	10740
Qy	10741	CAGTATTTTATAAACATCTTCTACAAACTCACACATTTTAAAAACAACACTGTCCTC	10800
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Qy	10801	TAAATCCCAAATTTTTCATAAAC	10825
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RESULT      3
US-08-552-265-5
? Sequence 5, Application US/08652265
? Patent No. 6025130
? GENERAL INFORMATION:
? APPLICANT: Thomas, Winston J.
? APPLICANT: Drayna, Dennis T.
? APPLICANT: Feder, John N.
? APPLICANT: Gnirke, Andreas
? APPLICANT: Ruddy, David
? APPLICANT: Tsuchihashi, Zenta
? APPLICANT: Wolff, Roger K.
? TITLE OF INVENTION: Hereditary
? NUMBER OF SEQUENCES: 44
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Towns
? STREET: Two Embarcadero Center
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-D

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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/652,265

FILING DATE: 23-MAY-1996

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 17957-000500

TELEPHONE: (415) 576-0200

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INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 10825 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: join(361..436, 3762..4025, 4235..4510, 5606..5881,

LOCATION: 6040..6153, 7107..7147)

OTHER INFORMATION: /product= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: mutation"

OTHER INFORMATION: /note= "Hereditary Hemochromatosis (HH)

OTHER INFORMATION: gene 24d2 allele"

FEATURE:

NAME/KEY: -

LOCATION: 140..7319

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: 24d2 allele cdna (SEQ ID NO:11)"

FEATURE:

NAME/KEY: -

LOCATION: 3852..3891

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d2(G) allele (SEQ ID NO:42)"

FEATURE:

NAME/KEY: -

LOCATION: 5507..6023

OTHER INFORMATION: /note= "start and stop positions for

OTHER INFORMATION: genomic sequence surrounding variant

OTHER INFORMATION: for 24d1(G) allele (SEQ ID NO:20)"

FEATURE:

NAME/KEY: allele

LOCATION: replace(3872, "g")

OTHER INFORMATION: /phenotype= "Hereditary Hemochromatosis

OTHER INFORMATION:

OTHER INFORMATION: /label= 24d2

US-08-652-265-5

Query Match 100.0%; Score 10823; DB 3; Length 10825;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy	61	AATATCTAAAGTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACCCCT	120
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Qy	121	TCAGGATTTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAACGACGACCTT	180
Db	121	TCAGGATTTAAAAACCAAGGGGACACTGGATCAGCTAGTGTTCACAACGACGACCTT	180
Qy	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGCTGTTTCCACCAAGGAATT	240
Db	181	CTGCTGTAGGAGAGAGAACTAAAGTTCGAAAGACCTGCTGTTTCCACCAAGGAATT	240

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Qy	361	ATGGGCGCGGAGCGGCGGCTTCTCCTCTCTGATGCTTTTGCAGACCGCGGTCTTG	420
Db	361	ATGGGCGCGGAGCGGCGGCTTCTCCTCTCTGATGCTTTTGCAGACCGCGGTCTTG	420
Qy	421	CAGGGGCGCTTGCTGCTGAGTCCGAGGGCTCGGGGAACTAGGGCGCGGGGGT	480
Db	421	CAGGGGCGCTTGCTGCTGAGTCCGAGGGCTCGGGGAACTAGGGCGCGGGGGT	480
Qy	481	GAAAAATCGAAACTAGCTTTTCTGCGCTTGGAGTTTGAAGTAACTTTGGAGGACCTGC	540
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Qy	601	CTACCACTGAACTCAGATAGGGGTCCTCGCCCGCAGGACCTGCCCTCCCGCGCTGT	660
Db	601	CTACCACTGAACTCAGATAGGGGTCCTCGCCCGCAGGACCTGCCCTCCCGCGCTGT	660
Qy	661	CCGGGCTCTCGGAGTGACTTTTGAACCCGCCACCTCCCTCCCGCAACTAGAACTCTTT	720
Db	661	CCGGGCTCTCGGAGTGACTTTTGAACCCGCCACCTCCCTCCCGCAACTAGAACTCTTT	720
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Qy	841	AAGTTCTTCCCTGAGTGTTCGCGAGAAGCTGAGCAAAACCCACAGCAGATCCGACGG	900
Db	841	AAGTTCTTCCCTGAGTGTTCGCGAGAAGCTGAGCAAAACCCACAGCAGATCCGACGG	900
Qy	901	GGTTCCACCTCAGAACGAAATGGTGGGCGGTGGGGCGCGAAAGAGTGGGTTGGGA	960
Db	901	GGTTCCACCTCAGAACGAAATGGTGGGCGGTGGGGCGCGAAAGAGTGGGTTGGGA	960
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Db	1021	GGAGGCTCCTGAGAGGCTTACCTCGGGCTTTCCCGCTTTCCCGCAATTTCTTTT	1080
Qy	1081	GCTGTGAAAATTAAGTATATGTTAGTTTGAAGTGAAGTGAACAAATCTCTTTTGG	1140
Db	1081	GCTGTGAAAATTAAGTATATGTTAGTTTGAAGTGAAGTGAACAAATCTCTTTTGG	1140
Qy	1141	CTAGGCTTTTATTTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Db	1141	CTAGGCTTTTATTTGCAATGCTGTGTAATTAAGAGGCTCTCTACAAAGTACTGA	1200
Qy	1201	TAAATGAACATGAAGCAATGCACTTCTAAGTTACATTCATATCTAATTTGA	1260
Db	1201	TAAATGAACATGAAGCAATGCACTTCTAAGTTACATTCATATCTAATTTGA	1260
Qy	1261	TTTTTCACTAGGAGGAGGAGTAAATTAACGTTTATTTTACTAGAGTTAACT	1320
Db	1261	TTTTTCACTAGGAGGAGGAGTAAATTAACGTTTATTTTACTAGAGTTAACT	1320

Qy	5701	AAGTGGCTGAAGGATAACGACGCCAAATGATGTCGAAGAGTTTGGAACTTAAGACGCTATTG	5760
Db	5701		5760
Qy	5761	CCCAATGGGGATGGGCACTTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGGAAGAG	5820
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Qy	5821	CAGAGATATACCTNCCAGGTGGACACCCAGGCCCTGGATCAGCGCCCTCAATGTGATCTGG	5880
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Qy	5881	GGTATCTGACTCATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGTTGAGAGGAGTCC	5940
Db	5881	GGTATCTGACTCATGAGAGCCAGGAGCTGAGAAAATCTATTGGGGTTGAGAGGAGTCC	5940
Qy	5941	TGAGGAGGTAATTATTGGCAGTCAGATGAGGATCTGCTCTTTGTAGGGGTGGGCTGAGG	6000
Db	5941	TGAGGAGGTAATTATTGGCAGTCAGATGAGGATCTGCTCTTTGTAGGGGTGGGCTGAGG	6000
Qy	6001	GTGGCAATCAAAAGGCTTTAACTTGCTTTTCTGTTTTTAGAGCCCTCACGCTCTGGGCACCC	6060
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Qy	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCGTCATCTTGTTTCATTGGAAATT	6120
Db	6061	TAGTCATTGGAGTCATCAGTGGAAATGCTGTTTTTGTGTCGTCATCTTGTTTCATTGGAAATT	6120
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Qy	6181	TACTACTCTGCCCAAGGSCACAGTGGAAAGGGGACAGAGGGATCTGGCATCCATGGG	6240
Db	6181	TAGTACTCTGCCCAAGGSCACAGTGGAAAGGGGACAGAGGGATCTGGCATCCATGGG	6240
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Qy	6301	AATGGTTCTCCCCAGAACTCTTAATTCAAACAACATCTTCAGACACCTACTAT	6360
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Qy	6661	GAGTATAAGGCATACCTGGGAGATTAGAAATAATTAAGTCTTAACCTGAGTTTCGGT	6720
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Qy	6781	GAATCAGAAAGAACCCAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTGGGTTATGA	6840

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Qy	6841	TCACTGGGTGTCTATTGAAGGATCCTAAAGAAAGGAGGACCACGATCTCCCTTATATGGTG	6900
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Qy	7201	GGGAGTCATTTATGAGCTCTTCATCTTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
Db	7201	GGGAGTCATTTATGAGCTCTTCATCTTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
Qy	7261	GCCTGACGAACTCCTTGATTTTAGCCCTCTCTGTGTTCAATTTCTCTCAAAAAGATTTCCCAT	7320
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Qy	7321	TTAGGTTCTTGAGTTCCTGCATCCCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACCTG	7380
Db	7321	TTAGGTTCTTGAGTTCCTGCATCCCGGTGATCCCTAGCTGTGACCTCTCCCTGGAACCTG	7380
Qy	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCCGTCACTCTCAGAG	7440
Db	7381	TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCCGTCACTCTCAGAG	7440
Qy	7441	ACATACACCTATGTCATTTTCATTTCCATTTCTTTTGAAGAGGAGCTCCTTAAATTTGGGGGA	7500
Db	7441	ACATACACCTATGTCATTTTCATTTCCATTTCTTTTGAAGAGGAGCTCCTTAAATTTGGGGGA	7500
Qy	7501	CTTACATGATTTCATTTTAACATCTGAGAAAAGCTTTGAACCCCTGGGACGTGGCTAGTCAT	7560
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Db	7561	AACCTTACCAGATTTTACACATGATCTATGCATTTTCTGACCCGTTCAACTTTTCCCT	7620
Qy	7621	TTGAATCCTCTCTGTGTTTACCAGTAACTCATCTGTCAACCAAGCCTTGGGGATCTTTC	7680
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APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Guirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolf, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10825 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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OTHER INFORMATION: (unaffected)"
OTHER INFORMATION: /label= 24d1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 10823; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 241 TTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGTGACTTCTGAGCCATCCCG 300
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QY 601 CTACCCTGAACCTGCAGATAGGGGTCCCTCGCCCCAGGACCTGCCCTCCCTCCCGGCTGT 660

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Db 1501 CTAGCTGATCCACATTTTACATGACAAAGATGAGGCATGGCAGCCCTGCTTCCTGG 1560
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Db 1801 GATGACAATAGCAATGAGCAGAGAAGATATACAACTACAGAAATCATGGTGTGTGA 1860
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Db 1861 SAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGACATGAAGGA 1920
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QY 1921 AATAAGAATGATATTGACTGGGAGCAGTATTTCOCAGGCAAACTGAGTGGGCCCTGGCAAG 1980
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Db 2221 AATAACAAGTGTGCTGGGAGTAGAGCCAGAAAGTAGGTAAATGGGCTCAGAGAGGA 2280
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QY 2461 AGGTAGTGGAGTGGGCTGGGAGCAAGAAAGGAGTGACAAACCAATGCTCTCCCTGAA 2520
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Db 2521 TATATTTCTGAAGAACTTCTGAAGGATCTATGTTGTGTGAGAGAAAGAAATGG 2580
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QY 2581 CTGGGTGTAGTACTCATGCCAAGGAGGAGCCAAAGGAGCAGATTCCTGAGCTCAGGA 2640
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QY 2641 GTTCAAGACCGCTGGGCAACACAGCAAAACCCCTCTCTACAAAAAATACAAAAATTA 2700
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QY 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGAGGCTGAGGTGGAGGTA 2760
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Db 2701 GCTGGGTGTGGTGGCATGCACCTGTGATCCTAGCTACTCGGAGGCTGAGGTGGAGGTA 2760
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QY 2761 TTGCTTTGAGCCCAAGGAAGTTGAGGCTGCAGTGCAGCCATGATGCTGCTACTTACTTACG 2820
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Db 2761 TTGCTTTGAGCCCAAGGAAGTTGAGGCTGCAGTGCAGCCATGATGCTGCTACTTACTTACG 2820
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Qy	2821	CTAGTGCACAGCAAGACCCCTGTCTCCCCTGACCCCTGAAAAGAGAAAGTAAAGT	2880
Db	2821	CTAGTGCACAGCAAGACCCCTGTCTCCCCTGACCCCTGAAAAGAGAAAGTAAAGT	2880
Qy	2881	TGACTTTGTTCTTTATTTTAAATTTATTTGGCCTGAGCAGTGGGTAAATTGGCAATGCCAT	2940
Db	2881	TGACTTTGTTCTTTATTTTAAATTTATTTGGCCTGAGCAGTGGGTAAATTGGCAATGCCAT	2940
Qy	2941	TTCTGAGATGTTGAAGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Db	2941	TTCTGAGATGTTGAAGCAGAGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG	3000
Qy	3001	GGACATGTTAAGTTTGAGATTTCCAGTTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Db	3001	GGACATGTTAAGTTTGAGATTTCCAGTTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT	3060
Qy	3061	CAGTGTAAAGAAATTCAGSACCAGGCTGGGCACGGTGGCTCACTTCTGTAATCCGACACT	3120
Db	3061	CAGTGTAAAGAAATTCAGSACCAGGCTGGGCACGGTGGCTCACTTCTGTAATCCGACACT	3120
Qy	3121	TTGGTGGCTGAGGCAGGTAGATCAATTCAGGTCAGSAGTTTGAGACAAGCTTGGCCACA	3180
Db	3121	TTGGTGGCTGAGGCAGGTAGATCAATTCAGGTCAGSAGTTTGAGACAAGCTTGGCCACA	3180
Qy	3181	TGGTGAACCCCATGCTCTACTAAAAATACAAAAATAGCCCTGGTGGCGCACGGCT	3240
Db	3181	TGGTGAACCCCATGCTCTACTAAAAATACAAAAATAGCCCTGGTGGCGCACGGCT	3240
Qy	3241	ATAGTCCAGGTTTTCAGGAGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGTGCAGG	3300
Db	3241	ATAGTCCAGGTTTTCAGGAGCTTAGGTAGAGAAATCCCTTGAACCCAGGAGTGCAGG	3300
Qy	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGCAGCTGT	3360
Db	3301	TTGCAGTGCAGCTGAGATTGTGCCACTGCACCTCCAGCCTGGGTGATAGAGTGCAGCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAACTGAAGAAATATTCCCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAACTGAAGAAATATTCCCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGCCCTGAGCACCACCTCTCTGAGTTCAACTACCATGGCTAGACACACCTTAAC	3480
Db	3421	TCTAATTTGCCCTGAGCACCACCTCTCTGAGTTCAACTACCATGGCTAGACACACCTTAAC	3480
Qy	3481	ATTTCTAGAAATCCACCACCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
Db	3481	ATTTCTAGAAATCCACCACCTTTAGTGGAGTCTGTCTAATCATGAGTATTGGAATAGGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGTGGCAGCCACCTGTGGCAGAGAAAGACACAAAGAAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGTGGCAGCCACCTGTGGCAGAGAAAGACACAAAGAAAGAGC	3600
Qy	3601	ACCCAGGACTGTCAATATGAAGAAAGACAGGACTGCAACTCACCCTTCACAAATGAGGA	3660
Db	3601	ACCCAGGACTGTCAATATGAAGAAAGACAGGACTGCAACTCACCCTTCACAAATGAGGA	3660
Qy	3661	CCAGACACAGCTCATGATGAGTTGATGCAGTGTGGAGCCTCAACATCCTGCTCCC	3720
Db	3661	CCAGACACAGCTCATGATGAGTTGATGCAGTGTGGAGCCTCAACATCCTGCTCCC	3720
Qy	3721	CTCCTACTACATGTTTAAAGGCCTGTGCTGTCTCCAGGTTTCACATCTCTGCACATA	3780
Db	3721	CTCCTACTACATGTTTAAAGGCCTGTGCTGTCTCCAGGTTTCACATCTCTGCACATA	3780
Qy	3781	CCTCTTCATGGGTGCCTCAGACAGGACCTTGCTCTTCCCTGTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTTCATGGGTGCCTCAGACAGGACCTTGCTCTTCCCTGTTTGAAGCTTTGGGCTA	3840
Qy	3841	CGTGGATGACACAGCTGTTCGTGTTCTATGATNATGAGAGTCGCGGTGTGGAGCCCCGAAC	3900
Db	3841	CGTGGATGACACAGCTGTTCGTGTTCTATGATNATGAGAGTCGCGGTGTGGAGCCCCGAAC	3900
Qy	3901	TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTAGATCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTAGAAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCTAGATCTGAA	3960
Qy	3961	AGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGAAAAATCACACCCACAG	4020
Db	3961	AGGTGGGATCACATGTTCACTGTTGACTTCTGGACTATTATGAAAAATCACACCCACAG	4020
Qy	4021	CAAGGATGTGGAGAGGGGCCCTCACCTTCTGAGGTTGTGCAGAGCTTTTCATCTTTTC	4080
Db	4021	CAAGGATGTGGAGAGGGGCCCTCACCTTCTGAGGTTGTGCAGAGCTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTTGAAGAAACAGCTGGAAGTCTGAGGCTTGTGGGAGCAGGAGAGGGGAAG	4140
Db	4081	ATGCATCTTTGAAGAAACAGCTGGAAGTCTGAGGCTTGTGGGAGCAGGAGAGGGGAAG	4140
Qy	4141	GAATTTGCTTCTGAGATCAATTTGGTCCCTGGGATGCTGGAATAAGGACCTATTCCCT	4200
Db	4141	GAATTTGCTTCTGAGATCAATTTGGTCCCTGGGATGCTGGAATAAGGACCTATTCCCT	4200
Qy	4201	TGGTTGCAGTTTAAACAAGCTGGGGATTTTTCCAGAGTCCCACACCCCTGCAGGTCATCTG	4260
Db	4201	TGGTTGCAGTTTAAACAAGCTGGGGATTTTTCCAGAGTCCCACACCCCTGCAGGTCATCTG	4260
Qy	4261	GGCTGTAATTCGAAGAGACAAACAGTACCGAGGCTACTCGAACTACGGGTATGATGGG	4320
Db	4261	GGCTGTAATTCGAAGAGACAAACAGTACCGAGGCTACTCGAACTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACCTTTGAATTCGCCCCTGACACACTGAGATTGGAGAGCAGCAGAACCCAGGCC	4380
Db	4321	CAGGACCACCTTTGAATTCGCCCCTGACACACTGAGATTGGAGAGCAGCAGAACCCAGGCC	4380
Qy	4381	TGGCCCCCAACGCTGAGTGGGAAAGGACAAAGATTTCGGGCCAGGCAGAACAGGCGCTAC	4440
Db	4381	TGGCCCCCAACGCTGAGTGGGAAAGGACAAAGATTTCGGGCCAGGCAGAACAGGCGCTAC	4440
Qy	4441	CTGGAGAGGGACTGCCTCCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTTTGTG	4500
Db	4441	CTGGAGAGGGACTGCCTCCACAGCTGCAGCAGTTGCTGGAGCTGGGGAGAGGTTTGTG	4500
Qy	4501	GACCAACAGGTTAGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAGGTTAGTGGAAACACACTTCTGCCCTATATCTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC	4620
Db	4561	AGGTTGCAGGGCACGGAATCCCTGGTTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC	4620
Qy	4621	TCCAAATTTCTGGAGGGACTTCTCAATCCTAGAGTCTCTACCTTATATTCAGATGTA	4680
Db	4621	TCCAAATTTCTGGAGGGACTTCTCAATCCTAGAGTCTCTACCTTATATTCAGATGTA	4680
Qy	4681	TGAGACAGCCACAAGTCATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	4740
Db	4681	TGAGACAGCCACAAGTCATGGGTTTAAATTTCTTTTCTCCATGCATATGGCTCAAGGGAA	474

QY	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
Db	7201	GGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGTTGAACCTAAACATAGAAATT	7260
QY	7261	GCCTGACGAACTCCTTGATTTTATGACCTTCTCTGTTTCATTTCCCTCAAAAAGATTCCCAT	7320
Db	7261	GCCTGACGAACTCCTTGATTTTATGACCTTCTCTGTTTCATTTCCCTCAAAAAGATTCCCAT	7320
QY	7321	TTAGGTTTCTGAGTTCCTGCGATGCCGGTGATCCCTAGCTGAGACCTCTCCCTGGAACTG	7380
Db	7321	TTAGGTTTCTGAGTTCCTGCGATGCCGGTGATCCCTAGCTGAGACCTCTCCCTGGAACTG	7380
QY	7381	TCCTCATGAACCTCAAGCTGCATAGAGGCTTCCTTCATTTCTCCTCCGCTACCTCAGAG	7440
Db	7381	TCCTCATGAACCTCAAGCTGCATAGAGGCTTCCTTCATTTCTCCTCCGCTACCTCAGAG	7440
QY	7441	ACATACACCTATGTCATTTCTTCATTTTGGAGAGAGACTCCTTAAATTTGGGGA	7500
Db	7441	ACATACACCTATGTCATTTCTTCATTTTGGAGAGAGACTCCTTAAATTTGGGGA	7500
QY	7501	CTTACATGATTCAATTTTAACTCTCAGAAAAAGCTTGAACCTGGGACGTGGCTAGTCAAT	7560
Db	7501	CTTACATGATTCAATTTTAACTCTCAGAAAAAGCTTGAACCTGGGACGTGGCTAGTCAAT	7560
QY	7561	AACCTTACCAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTTCAACTTTTCCCT	7620
Db	7561	AACCTTACCAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTTCAACTTTTCCCT	7620
QY	7621	TTGAATCCTCTCTGTTTACCCAGTAACCTCACTGCTGCACCAAGCCTTGGGATTTCTTC	7680
Db	7621	TTGAATCCTCTCTGTTTACCCAGTAACCTCACTGCTGCACCAAGCCTTGGGATTTCTTC	7680
QY	7681	CATCTGATTGTGATGTGAGTTTCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG	7740
Db	7681	CATCTGATTGTGATGTGAGTTTCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG	7740
QY	7741	GCACCTGTCCCGAAAAAGCATCATGGCTATCTGCGGTAGTAGTATGATGGGTGTTTTTACG	7800
Db	7741	GCACCTGTCCCGAAAAAGCATCATGGCTATCTGCGGTAGTAGTATGATGGGTGTTTTTACG	7800
QY	7801	AGGTGAGGAGCAAAATCTTTGAAAGGGTGTGAAAGAGGCTTTTTTCTCAATTGGCATGA	7860
Db	7801	AGGTGAGGAGCAAAATCTTTGAAAGGGTGTGAAAGAGGCTTTTTTCTCAATTGGCATGA	7860
QY	7861	AGTGTGCATACAGATTTGCAAGTTTAATGTTGCCTTCATTTGGATGCTACTCTAGTAT	7920
Db	7861	AGTGTGCATACAGATTTGCAAGTTTAATGTTGCCTTCATTTGGATGCTACTCTAGTAT	7920
QY	7921	TCCAGACCTCAGAAATCACAATAATTTTCTACCTGGTCTCTCTGTTGTAATAATGAAA	7980
Db	7921	TCCAGACCTCAGAAATCACAATAATTTTCTACCTGGTCTCTCTGTTGTAATAATGAAA	7980
QY	7981	ATTATGATAAGGATGATAAAGCACTTACTTCGTCTCCGACTCTTCTGAGCACTACTTA	8040
Db	7981	ATTATGATAAGGATGATAAAGCACTTACTTCGTCTCCGACTCTTCTGAGCACTACTTA	8040
QY	8041	CATGCATCTACTGCATGCACCTCTTCAACAATAATTTCTATGAGATAGTACTATTATCCCAT	8100
Db	8041	CATGCATCTACTGCATGCACCTCTTCAACAATAATTTCTATGAGATAGTACTATTATCCCAT	8100
QY	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCCGGGACGGTGGCTCAGCGCTGTAATCCC	8160
Db	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCCGGGACGGTGGCTCAGCGCTGTAATCCC	8160
QY	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCAGAGGTTCAGAGATCAGAGACCTTCTGGC	8220
Db	8161	AGCACTTTGGGAGGCCAAAGCGGGTGGATCAGAGGTTCAGAGATCAGAGACCTTCTGGC	8220
QY	8221	TAAATGTTGTAACCCCATCTCTTAATAAAAAATACAAAAAATTTAGCTGGCGCTGGTGGCAG	8280
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[illegible]

[illegible]

Db	10441	CGCTGAGGGTTTCCTCGAAGGTAAAGGAATAAGAAATGGGTGGAGGGGGCTGCACCTGGAA	10500
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Db	10501	ATCACTTTGTAGAGAAAAGCCCCCTGAAAATTTTGAAAAACAACAAGAACTACTTACCAG	10560
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Db	10561	CTATTTGAAATTCGCTGGAAATCACAGGCCATTGCTGAGCTGCCTGAACTGGGAACAACAAG	10620
Qy	10621	AAGGAAAACAACACACTCTGTATATCATCTTCAAGTCAAGTACAGCAGCTGATTTGAGGACTGC	10680
Db	10621	AAGGAAAACAACACACTCTGTATATCATCTTCAAGTCAAGTACAGCAGCTGATTTGAGGACTGC	10680
Qy	10681	TGAGAGGTACAGGCCAAAATTCATTGCTGATATATAAATGTCATCTTATAAATACTGT	10740
Db	10681	TGAGAGGTACAGGCCAAAATTCATTGCTGATATATAAATGTCATCTTATAAATACTGT	10740
Qy	10741	CAGTATTTTATAAACAATCTTTCACAAACTCACACACATTTAAAAACAACAACACTGTCTC	10800
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RESULT 6			
US-08-834-497A-3			
; Sequence 3, Application US/08834497A			
; Patent No. 6140305			
; GENERAL INFORMATION:			
; APPLICANT: Thomas, Winston J.			
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; APPLICANT: Feder, John N.			
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; APPLICANT: Ruddy, David			
; APPLICANT: Tsuchihashi, Zenta			
; APPLICANT: Wolff, Roger K.			
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS			
; NUMBER OF SEQUENCES: 76			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Pennie & Edmonds LLP			
; STREET: 1155 Avenue of the Americas			
; CITY: New York			
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; ZIP: 10036-2811			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: Windows 95			
; SOFTWARE: FastSEQ for Windows Version 2.0b			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/834,497A			
; FILING DATE: 04-APR-1997			
; CLASSIFICATION: 514			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/632,673			
; FILING DATE: 16-APR-1996			
; CLASSIFICATION: 514			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: US 08/630,912			
; FILING DATE: 04-APR-1996			
; CLASSIFICATION: 514			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Poissant, Brian M.			
; REGISTRATION NUMBER: 28,462			
; REFERENCE/DOCKET NUMBER: 8907-0056-999			

QY 1441 TGTAGCAGTGTCTGTGGGTACACGCCGCCCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCAGTGTCTGTGGGTACACGCCGCCCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
QY 1501 CTACGTGTATCCACATTTTACACATGACAAGAAATGAGGCATGGCAGGCCTGCTTCCTGG 1560
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Db 1621 TATGATTTCTTAAACATCACACTGCATTAGAGGTTGAATAATAAATTTTCATGTTGAGCAG 1680
QY 1681 AAATATTCAATTTTACAAGTGTAAATGAGTCCCAAGCATGTTGTCACACTGTTCAAGCCC 1740
Db 1681 AAATATTCAATTTTACAAGTGTAAATGAGTCCCAAGCATGTTGTCACACTGTTCAAGCCC 1740
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Db 1741 CAAGGAGAGCAGCGGAAACAAGTCTTTACCCCTTTTGATATTTTGCATTTCTAGTGGGAGA 1800
QY 1801 GATGACAAATAGCAAAATGAGCAGAAGATATACAACATCAGGAAATCATGGGTGTTGTA 1860
Db 1801 GATGACAAATAGCAAAATGAGCAGAAGATATACAACATCAGGAAATCATGGGTGTTGTA 1860
QY 1861 GAAGCAGAGAAGTCAGGCAAGTCACTCTGGGCTGACACTTGAGCAGAGCATGAAGGA 1920
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QY 1921 AATAAGAATGATATTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGCCCTGGCAAG 1980
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Db 5581 CTCATCT 5640
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RESULT 7
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; Sequence 5, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A

; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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; OTHER INFORMATION: /label= 24d2
; US-08-834-497A-5

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Db 61 AATATCTAAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACACACCCCT 120
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QY	3361	CTCAAAAAAAAAAAAAAAAAAAAAAATGAGGAATTATTCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAATGAGGAATTATTCTCAGGATTTGGG	3420
QY	3421	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCACCTACCATTGGCTAGCACACCTTAAC	3480
Db	3421	TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCACCTACCATTGGCTAGCACACCTTAAC	3480
QY	3481	ATTTTCTAGAAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGATGATTGGAATAGGAT	3540
Db	3481	ATTTTCTAGAAATCCACCAGCTTTAGTGGAGTCTGTCTAATCATGATGATTGGAATAGGAT	3540
QY	3541	CTGGGGCAGTGAGGGGGTGGCAGCACCGTGTGGCAGAGAAAAGCACAAAGGAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGGTGGCAGCACCGTGTGGCAGAGAAAAGCACAAAGGAAGAGC	3600
QY	3601	ACCAGGACGTGCATATGGAAGAAGACAGGACTGCACTCACCTTCACAANAATGAGGA	3660
Db	3601	ACCAGGACGTGCATATGGAAGAAGACAGGACTGCACTCACCTTCACAANAATGAGGA	3660
QY	3661	CCAGACAGCTGATGTTAGTGTGATGACAGTGTGTGGAGCCCTCAACATCCTGCTCCC	3720
Db	3661	CCAGACAGCTGATGTTAGTGTGATGACAGTGTGTGGAGCCCTCAACATCCTGCTCCC	3720
QY	3721	CTCTACTACACATGGTTAAGGCTGTGGTCTGTCTCCAGGTTCCAGCTCTCTGCACATA	3780
Db	3721	CTCTACTACACATGGTTAAGGCTGTGGTCTGTCTCCAGGTTCCAGCTCTCTGCACATA	3780
QY	3781	CCTCTCATGGTGCCFCAGACGAGCACTTGGTCTTTCTTCTTTGAAGCTTTGGGCTA	3840
Db	3781	CCTCTCATGGTGCCFCAGACGAGCACTTGGTCTTTCTTCTTTGAAGCTTTGGGCTA	3840
QY	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCCCGTGTGGAGCCCCGAAC	3900
Db	3841	CGTGGATGACCAGCTGTTCGTGTTCTATGATNATGAGAGTCCCGTGTGGAGCCCCGAAC	3900
QY	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGTCAGTCTGAGTCTGAA	3960
Db	3901	TCCATGGGTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGTCAGTCTGAGTCTGAA	3960
QY	3961	AGGTGGGATCACATGTTCACTGTTGACATCTCGGACTATTATGGAANAATCACACCACAG	4020
Db	3961	AGGTGGGATCACATGTTCACTGTTGACATCTCGGACTATTATGGAANAATCACACCACAG	4020
QY	4021	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGGTTGTCCAGAGCTTTTCATCTTTTC	4080
Db	4021	CAAGGGTATGTGGAGAGGGGCCCTACCTTCCTGAGGTTGTCCAGAGCTTTTCATCTTTTC	4080
QY	4081	ATGCATCTTGAAGAAACAGCTGGAAAGTCTGAGGCTTTGTGGGAGCAGGGAAGGGAAG	4140
Db	4081	ATGCATCTTGAAGAAACAGCTGGAAAGTCTGAGGCTTTGTGGGAGCAGGGAAGGGAAG	4140
QY	4141	GAAATTCCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGNAATAGGACCTATTCCCTT	4200
Db	4141	GAAATTCCTTCCTGAGATCATTTGGTCCTTGGGGATGGTGGNAATAGGAGCTATTCCCTT	4200
QY	4201	TGGTTGCAGTTAACAGGCTGGGGATTTTTCCAGAGTCCACACCTCGCAGGTCACTCGT	4260
Db	4201	TGGTTGCAGTTAACAGGCTGGGGATTTTTCCAGAGTCCACACCTCGCAGGTCACTCGT	4260
QY	4261	GGCTGTGAATGCAAGAAGACAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAATGCAAGAAGACAACAGTACCGAGGCTACTGGAAGTACGGGTATGATGGG	4320
QY	4321	CAGACACACCTTGAAATCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAGGGCC	4380
Db	4321	CAGACACACCTTGAAATCTGCCCTGACACACTGGATTGGAGAGCAGCAACCCAGGGCC	4380
QY	4381	TGGGCCACCAAGCTGGAGTGGGAAGGCACAGATTCCGGCCAGCAGACAGGGCCCTAC	4440
Db	4381	TGGGCCACCAAGCTGGAGTGGGAAGGCACAGATTCCGGCCAGCAGACAGGGCCCTAC	4440
QY	4441	CTGAGAGGGACCTGCCCTGCACAGCTGCACAGTTCCTGGAGCTGGGAGAGGTTTGTG	4500

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Db 4441 CTGAGAGGACTGCCCTGCACAGCTGCAGCAGTTCTGGAGCTGGGAGAGGTGTTTG 4500
QY GACCAACAAGGTATGTTGGAACACACACTTCTGCCCTATATACTTCTAGTGGCAGAGTGGAGG 4560
Db 4501 GACCAACAAGGTATGTTGGAACACACACTTCTGCCCTATATACTTCTAGTGGCAGAGTGGAGG 4560
QY AGTTGCAGGGCAGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC 4620
Db 4561 AGTTGCAGGGCAGGAATCCCTGGTGGAGTTTCAGAGGTGGCTGAGGCTGTGTCCTC 4620
QY TCCAAATTCGGGAAGGGACTTCTCAATCCCTAGAGTCTTACCCTATATAATTCAGATGTA 4680
Db 4621 TCCAAATTCGGGAAGGGACTTCTCAATCCCTAGAGTCTTACCCTATATAATTCAGATGTA 4680
QY TGAGACAGCCACAAGTCATGGGTTTAAATTCCTTCCATGCATATGGCTCAAAAGGGAA 4740
Db 4681 TGAGACAGCCACAAGTCATGGGTTTAAATTCCTTCCATGCATATGGCTCAAAAGGGAA 4740
QY GTGTCTATGGCCCTTCTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA 4800
Db 4741 GTGTCTATGGCCCTTCTCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTTAA 4800
QY AAATTCAGAAATCTCAAGCCGGGCACGCTGGCTCACCCCTGTAATCCCGACACTTTGGG 4860
Db 4801 AAATTCAGAAATCTCAAGCCGGGCACGCTGGCTCACCCCTGTAATCCCGACACTTTGGG 4860
QY AGCCGAGGCGGTGTCACAAGCTCAGGAGTTTGAGACAGCCTGACCAACATGGTGAA 4920
Db 4861 AGCCGAGGCGGTGTCACAAGCTCAGGAGTTTGAGACAGCCTGACCAACATGGTGAA 4920
QY ACCGCTCTTAAAAAATAACAAAATTTAGTGTCTACAGTCAATGCGCACCTGTAGTCCCA 4980
Db 4921 ACCGCTCTTAAAAAATAACAAAATTTAGTGTCTACAGTCAATGCGCACCTGTAGTCCCA 4980
QY GCTAATTTGGAAGCTGAGGCAGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACCTGA 5040
Db 4981 GCTAATTTGGAAGCTGAGGCAGAGCATCGCTTGAACCTGGGAAGCGGAAGTTGCACCTGA 5040
QY GCCAAGATCGCGCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 5100
Db 5041 GCCAAGATCGCGCACTGCACTCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 5100
QY AAAAAAATAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACAGAGCAAA 5160
Db 5101 AAAAAAATAAGAGAAATTCAGAGATCTCAGCTATCATATGAATACAGAGCAAA 5160
QY ATATCAAGTCAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGTTAAAAAGTTCTTTTCAT 5220
Db 5161 ATATCAAGTCAGGCCACTTATCAGAGTAGAAGAAATCCTTTAGTTAAAAAGTTCTTTTCAT 5220
QY AGAACATAGCAATTAATCACTGAAAGCTACCTATCTTACAAGTCGCGTCTTATAACAATGC 5280
Db 5221 AGAACATAGCAATTAATCACTGAAAGCTACCTATCTTACAAGTCGCGTCTTATAACAATGC 5280
QY CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCATTAATCAATTTTCAATGCAATAA 5340
Db 5281 CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCATTAATCAATTTTCAATGCAATAA 5340
QY AGGCAATTTTATCTATCAGAACAAAGACATGGTAAACAGATATCTATATTTACATGTG 5400
Db 5341 AGGCAATTTTATCTATCAGAACAAAGACATGGTAAACAGATATCTATATTTACATGTG 5400
QY AGGAGAACAAAGCTGATCTGACTCTCTCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
Db 5401 AGGAGAACAAAGCTGATCTGACTCTCTCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
QY ACACAAATGGTGTCTCTCTGTAGCTGTGTTTTTTTCTGAAAAGGGTATTTCTCTCCTCC 5520
Db 5461 ACACAAATGGTGTCTCTCTGTAGCTGTGTTTTTTTCTGAAAAGGGTATTTCTCTCCTCC 5520
QY AACCTATAGAAGAGTGAAGTTCCAGTCTCTCGCAGGGTAAACAGATCCCTCTC 5580
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Db 5521 AACCTATAGAAGAGTGAAGTTCCAGTCTTCTCTGGCAAGGGTAAACAGATCCCTCTC 5580
QY CTCATCTCTCTCTTCTCTCAAGTGCCTCTTTTGGTGAAGTGACACATCATGTGACC 5640
Db 5581 CTCATCTCTCTCTTCTCTCAAGTGCCTCTTTTGGTGAAGTGACACATCATGTGACC 5640
QY TCTTCAGTGACCACTCTACGGGTGTCGGGCTTGAACCTACTACCTACCTACCTACCTACCT 5700
Db 5641 TCTTCAGTGACCACTCTACGGGTGTCGGGCTTGAACCTACTACCTACCTACCTACCTACCT 5700
QY AAGTGGCTGAAGGATAAGCAGCCAATGATGCCAAGAGTTTCGAACCTAAAGAGCTATTG 5760
Db 5701 AAGTGGCTGAAGGATAAGCAGCCAATGATGCCAAGAGTTTCGAACCTAAAGAGCTATTG 5760
QY CCCAATGGGGATGGGACCTACACAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 5820
Db 5761 CCCAATGGGGATGGGACCTACACAGGCTGGATAACCTTTGGCTGTACCCCTGGGGAAGAG 5820
QY CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGATCTGG 5880
Db 5821 CAGAGATATACGTNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGATCTGG 5880
QY GGTATGTCACTGATCAGAGCCAGAGCTGAGAAAATCTATTTGGGGTTGAGAGGAGTGCC 5940
Db 5881 GGTATGTCACTGATCAGAGCCAGAGCTGAGAAAATCTATTTGGGGTTGAGAGGAGTGCC 5940
QY TGAGAGATTAATTTAGCAGTGAGATCAGGATCTGCTCTTTTGGGGTTGAGGCTGAGG 6000
Db 5941 TGAGAGATTAATTTAGCAGTGAGATCAGGATCTGCTCTTTTGGGGTTGAGGCTGAGG 6000
QY GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTTTGTAGAGCCCTCAGGCTCTGGCACCC 6060
Db 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTCTGTTTGTAGAGCCCTCAGGCTCTGGCACCC 6060
QY TAGTCATTTGGAGTCACTAGTGAATTTGCTTTTGTCTGTCATCTTGTTCATTTGGAATTT 6120
Db 6061 TAGTCATTTGGAGTCACTAGTGAATTTGCTTTTGTCTGTCATCTTGTTCATTTGGAATTT 6120
QY TGTTCATTAATTTAAGGAAGAGGAGGGTTCAAGTGAAGTGAAGGAAGAGGGGAAAGTCTCT 6180
Db 6121 TGTTCATTAATTTAAGGAAGAGGAGGGTTCAAGTGAAGTGAAGGAAGAGGGGAAAGTCTCT 6180
QY TAGTACCTCTCCCCAGGCACAGTGGGAAGAGGGGACAGGGGATCTGGCATCCATGGG 6240
Db 6181 TAGTACCTCTCCCCAGGCACAGTGGGAAGAGGGGACAGGGGATCTGGCATCCATGGG 6240
QY AAGCATTTTCTCATTTATATTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT 6300
Db 6241 AAGCATTTTCTCATTTATATTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT 6300
QY AATGTTCTCCCCAGAATGAAGTCTCTTAATTCACAAACATCTTCAGAGCACCCTACTAT 6360
Db 6301 AATGTTCTCCCCAGAATGAAGTCTCTTAATTCACAAACATCTTCAGAGCACCCTACTAT 6360
QY TTTGCAAGAGCTGTTAAGGTAGTACAGGGCTTTGAGGTTGAGAGTCACTGTGGCTAT 6420
Db 6361 TTTGCAAGAGCTGTTAAGGTAGTACAGGGCTTTGAGGTTGAGAGTCACTGTGGCTAT 6420
QY TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATACAAAGTAAATGTAGTTAAAGAAG 6480
Db 6421 TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTGATACAAAGTAAATGTAGTTAAAGAAG 6480
QY ACCCATGAGGTCTTAAAGCAGGCAGGAAGCAATGCTTGGGTTTCAAGAGGAAGATG 6540
Db 6481 ACCCATGAGGTCTTAAAGCAGGCAGGAAGCAATGCTTGGGTTTCAAGAGGAAGATG 6540
QY ATCACAATTCAGCTGGGATCAAGATAGCTTCTGGATCTTGAAGGAGAGCTGATTTCCA 6600
Db 6541 ATCACAATTCAGCTGGGATCAAGATAGCTTCTGGATCTTGAAGGAGAGCTGATTTCCA 6600
QY TTAGTGTAGGTTGAAGATGATGGGAGGTCTACACAGCGGAGCAACCATGCTCAAGTAGGA 6660
Db 6601 TTAGTGTAGGTTGAAGATGATGGGAGGTCTACACAGCGGAGCAACCATGCTCAAGTAGGA 6660

Qy	6661	GAGTATAAGGCATAC	TGGGAGATTAGA	AATAA	TACTGTAC	CTTAAC	CTTGAG	CTTCGCT	TTCGCT	6720
Db	6661	GAGTATAAGGCATAC	TGGGAGATTAGA	AATAA	TACTGTAC	CTTAAC	CTTGAG	CTTCGCT	TTCGCT	6720
Qy	6721	AGCTATCACTACCA	ATATGCA	TTTCTT	ACCCCT	TGA	CACTCTG	TGCT	TAGG	6780
Db	6721	AGCTATCACTACCA	ATATGCA	TTTCTT	ACCCCT	TGA	CACTCTG	TGCT	TAGG	6780
Qy	6781	GAATCAGA	AAAGCCAG	CTCATAC	GAGTCCA	AGGTC	TTTGGG	ATATGG	GTATGA	6840
Db	6781	GAATCAGA	AAAGCCAG	CTCATAC	GAGTCCA	AGGTC	TTTGGG	ATATGG	GTATGA	6840
Qy	6841	TCAC	TGGGTG	CTATTA	GAAGTCT	TAA	GAGGAC	CA	GATCTT	6900
Db	6841	TCAC	TGGGTG	CTATTA	GAAGTCT	TAA	GAGGAC	CA	GATCTT	6900
Qy	6901	AA	TGTGTT	TAA	AGTTAG	ATGAG	GTGAG	GAG	CCAGT	6960
Db	6901	AA	TGTGTT	TAA	AGTTAG	ATGAG	GTGAG	GAG	CCAGT	6960
Qy	6961	TTCC	AGATGAG	AGATA	ATGGTCT	T	CAAT	TAGTCC	AGGTCT	7020
Db	6961	TTCC	AGATGAG	AGATA	ATGGTCT	T	CAAT	TAGTCC	AGGTCT	7020
Qy	7021	GTGA	TGAGG	AAATTA	GGA	GAGAG	AGAC	GAAGT	TGTC	7080
Db	7021	GTGA	TGAGG	AAATTA	GGA	GAGAG	AGAC	GAAGT	TGTC	7080
Qy	7081	CTTT	CTGGGT	CTTT	GTCTCC	ACAGG	AGG	CACTGG	GCAC	7140
Db	7081	CTTT	CTGGGT	CTTT	GTCTCC	ACAGG	AGG	CACTGG	GCAC	7140
Qy	7141	TGAG	TGAC	GCAG	CGCTG	CAG	ACTC	ACTGTG	GGAAG	7200
Db	7141	TGAG	TGAC	GCAG	CGCTG	CAG	ACTC	ACTGTG	GGAAG	7200
Qy	7201	GGG	AGTGCA	TTAT	GAG	CTTCA	TGTTT	CAG	GAGAG	7260
Db	7201	GGG	AGTGCA	TTAT	GAG	CTTCA	TGTTT	CAG	GAGAG	7260
Qy	7261	GCCT	GAG	GA	ACTCCT	CTG	CTGTT	CA	TTTCTC	7320
Db	7261	GCCT	GAG	GA	ACTCCT	CTG	CTGTT	CA	TTTCTC	7320
Qy	7321	TTAG	TTTCT	GAG	TTCT	CGAT	CGCG	TGAT	CCCT	7380
Db	7321	TTAG	TTTCT	GAG	TTCT	CGAT	CGCG	TGAT	CCCT	7380
Qy	7381	TC	CTCAT	G	AACTCA	AGCTG	CATCTAG	AGG	CTTCT	7440
Db	7381	TC	CTCAT	G	AACTCA	AGCTG	CATCTAG	AGG	CTTCT	7440
Qy	7441	ACAT	ACAC	CTAT	GTCA	TTTCA	TTTCA	TTT	TGGA	7500
Db	7441	ACAT	ACAC	CTAT	GTCA	TTTCA	TTTCA	TTT	TGGA	7500
Qy	7501	CTT	ACAT	GAT	CTAT	TTT	TA	CACTG	GAG	7560
Db	7501	CTT	ACAT	GAT	CTAT	TTT	TA	CACTG	GAG	7560
Qy	7561	AA	CTTAC	CA	GAT	TTT	TAC	ATG	ATCT	7620
Db	7561	AA	CTTAC	CA	GAT	TTT	TAC	ATG	ATCT	7620
Qy	7621	TT	GAAT	CT	CT	CT	GTG	T	TAC	7680
Db	7621	TT	GAAT	CT	CT	CT	GTG	T	TAC	7680
Qy	7681	CAT	CTG	AT	TG	AT	G	TG	AG	7740
Db	7681	CAT	CTG	AT	TG	AT	G	TG	AG	7740

Qy	7741	GCACCTGTC	CCAGAAAAG	CAATCATG	CGCTATCT	GTGGGTAG	TATGATG	GGTGTTT	TAGC	7800	
Db	7741	GCACCTGTC	CCAGAAAAG	CAATCATG	CGCTATCT	GTGGGTAG	TATGATG	GGTGTTT	TAGC	7800	
Qy	7801	AGGTAGGAG	CAAAATCT	TGAAAGGG	TTGTGAAGAG	CGTGT	TTTTTCT	TAATGGCAT	GA	7860	
Db	7801	AGGTAGGAG	CAAAATCT	TGAAAGGG	TTGTGAAGAG	CGTGT	TTTTTCT	TAATGGCAT	GA	7860	
Qy	7861	AGGTGTCAT	ACAGATTG	GCAAGTTA	TGFGCCCT	TCATTTG	GGATGCT	CTACTCTAG	TAT	7920	
Db	7861	AGGTGTCAT	ACAGATTG	GCAAGTTA	TGFGCCCT	TCATTTG	GGATGCT	CTACTCTAG	TAT	7920	
Qy	7921	TCAGAGCT	CTGAAGAAT	CAACAATA	TTTCTAC	TCTGCTCT	CCTTGTTCT	GTATTAAT	CAAA	7980	
Db	7921	TCAGAGCT	CTGAAGAAT	CAACAATA	TTTCTAC	TCTGCTCT	CCTTGTTCT	GTATTAAT	CAAA	7980	
Qy	7981	ATTATGATA	AGGATGATA	AAAGCACT	TACTCGT	GTCCGACT	CTCTCTGAG	CACCTACT	TTA	8040	
Db	7981	ATTATGATA	AGGATGATA	AAAGCACT	TACTCGT	GTCCGACT	CTCTCTGAG	CACCTACT	TTA	8040	
Qy	8041	CATGCATT	ACTGCATG	CACTTCT	TACAAATA	TTCTAT	GAGATAGT	ACTATTA	TATCC	8100	
Db	8041	CATGCATT	ACTGCATG	CACTTCT	TACAAATA	TTCTAT	GAGATAGT	ACTATTA	TATCC	8100	
Qy	8101	TTCTTTTT	TTAAATGA	AGAAAGT	GAAGTAG	CGCGGCA	CGGTGGCT	TCAGCCCT	GTAAATCCC	8160	
Db	8101	TTCTTTTT	TTAAATGA	AGAAAGT	GAAGTAG	CGCGGCA	CGGTGGCT	TCAGCCCT	GTAAATCCC	8160	
Qy	8161	AGCACTTT	GGGAGGCC	CAAGCGGG	TGGATC	ACAGAGT	CAGAGATC	GAGACCT	CTTGCC	8220	
Db	8161	AGCACTTT	GGGAGGCC	CAAGCGGG	TGGATC	ACAGAGT	CAGAGATC	GAGACCT	CTTGCC	8220	
Qy	8221	TAACATG	GTGAAAC	CCCATCT	CTTAATA	AAAAAT	TACAAAAA	TTAGCT	GGCGCTGTGGCAG	8280	
Db	8221	TAACATG	GTGAAAC	CCCATCT	CTTAATA	AAAAAT	TACAAAAA	TTAGCT	GGCGCTGTGGCAG	8280	
Qy	8281	ACGCCT	GTAGTCC	CAGCTACT	CGGAAGG	CTGAGG	CAGAGAA	TGCGAT	GAACCCAGGAGG	8340	
Db	8281	ACGCCT	GTAGTCC	CAGCTACT	CGGAAGG	CTGAGG	CAGAGAA	TGCGAT	GAACCCAGGAGG	8340	
Qy	8341	CAGAGCT	TGCAGT	CAGCCGAG	TTTGC	GCACAT	GCACCTC	CAGCTAG	GTGACAGAGT	GAGA	8400
Db	8341	CAGAGCT	TGCAGT	CAGCCGAG	TTTGC	GCACAT	GCACCTC	CAGCTAG	GTGACAGAGT	GAGA	8400
Qy	8401	CTCCAT	CTCAAAAAA	TAAAAAT	TAAAAA	TAAAAA	TAAAAA	TAAAAA	TAAAAA	GAAGTGAAGTA	8460
Db	8401	CTCCAT	CTCAAAAAA	TAAAAAT	TAAAAA	TAAAAA	TAAAAA	TAAAAA	TAAAAA	GAAGTGAAGTA	8460
Qy	8461	TAGAGTAT	CTCATAGT	TTGTGTC	AGTATAG	AAACAG	GTCTTCA	ACCTCAGT	CAATCTG	ACCG	8520
Db	8461	TAGAGTAT	CTCATAGT	TTGTGTC	AGTATAG	AAACAG	GTCTTCA	ACCTCAGT	CAATCTG	ACCG	8520
Qy	8521	TTTGAT	ATCATCT	CAGACCA	CTACAT	CTCAGT	AGTTTAG	ATGCCCT	TAGAAATA	TAGAGAA	8580
Db	8521	TTTGAT	ATCATCT	CAGACCA	CTACAT	CTCAGT	AGTTTAG	ATGCCCT	TAGAAATA	TAGAGAA	8580
Qy	8581	GGAAGG	ATGGCTCT	TTCTTGT	CTCATGTG	TTTCTT	CTCAGT	GAGCTT	GAATC	ACAT	8640
Db	8581	GGAAGG	ATGGCTCT	TTCTTGT	CTCATGTG	TTTCTT	CTCAGT	GAGCTT	GAATC	ACAT	8640
Qy	8641	GAAGGG	AACAGC	AGAAAAA	CAACCA	CTGATCT	CAGCTGT	CATGTTC	CTTTAA	AAAGTC	8700
Db	8641	GAAGGG	AACAGC	AGAAAAA	CAACCA	CTGATCT	CAGCTGT	CATGTTC	CTTTAA	AAAGTC	8700
Qy	8701	CCTGAAG	GAAGGTC	TCTGGA	ATGTGAC	TTCCCT	CTGTGCT	CTCTTT	TGGCAT	TCA	8760
Db	8701	CCTGAAG	GAAGGTC	TCTGGA	ATGTGAC	TTCCCT	CTGTGCT	CTCTTT	TGGCAT	TCA	8760
Qy	8761	TTTCTT	CTGGAC	CCCTAC	CGAAGG	ACTGTA	TTTGGT	GGGACAG	CTAGT	GGCCCTGCTGGC	8820
Db	8761	TTTCTT	CTGGAC	CCCTAC	CGAAGG	ACTGTA	TTTGGT	GGGACAG	CTAGT	GGCCCTGCTGGC	8820
Qy	8821	TTTACAC	ACGGTGT	CTCCCT	TAGGCC	AGTGCCT	CTGGAGT	CAAGAACT	CTGTTGGT	ATTTC	8880

Db 8821 TFCACACAGGTGCTCCCTAGGCCAGTGCCTGGAGTCAGAACTCTGGTGTATTTTC 8880
QY COTCAATGAAGTGGAGTAAAGCTCTCTCATTTTGGATGGTAAATGAAGCCACCAAGTG 8940
Db 8881 CCTCAATGAAGTGGAGTAAAGCTCTCTCATTTTGGATGGTAAATGAAGCCACCAAGTG 8940
QY GCTTAGAGGATGCCAGGCTCCTCCATCGAGCCACTGGGGTCCGGTGCACATTTAAAAA 9000
Db 8941 GCTTAGAGGATGCCAGGCTCCTCCATCGAGCCACTGGGGTCCGGTGCACATTTAAAAA 9000
QY 9001 AAAATCTAACAGACATTCAGGAATTCAGTAATTCGGGAATTCAGTTCCACCATGTTCA 9060
Db 9001 AAAATCTAACAGACATTCAGGAATTCAGTAATTCGGGAATTCAGTTCCACCATGTTCA 9060
QY 9061 AAAGAGTCTTTTTTTTTTTTGGAGCTCTATTGCCAGGCTGGAGTGCATGSCATGAT 9120
Db 9061 AAAGAGTCTTTTTTTTTTTTGGAGCTCTATTGCCAGGCTGGAGTGCATGSCATGAT 9120
QY 9121 CTCGGCTCACGTGAACCTCTGCCCTCCAGGTTCAAGCGATTCCTCTGCTCAGCCTCCCA 9180
Db 9121 CTCGGCTCACGTGAACCTCTGCCCTCCAGGTTCAAGCGATTCCTCTGCTCAGCCTCCCA 9180
QY 9181 AGTAGCTGGGATTACAGCGGTGACACCACTGCGCCGCTAAATTTTGTATTTTAGTAGA 9240
Db 9181 AGTAGCTGGGATTACAGCGGTGACACCACTGCGCCGCTAAATTTTGTATTTTAGTAGA 9240
QY 9241 GACAGGTTTTCCACCATGTTGGCCAGGTGCTCGAACTCTCCTGACCTCGTGATCGGCC 9300
Db 9241 GACAGGTTTTCCACCATGTTGGCCAGGTGCTCGAACTCTCCTGACCTCGTGATCGGCC 9300
QY 9301 TGCCTCGCCCTCCCAAGTGTGATATACAGGTGTGAGCCACCCCTGCCAGCGTCAAA 9360
Db 9301 TGCCTCGCCCTCCCAAGTGTGATATACAGGTGTGAGCCACCCCTGCCAGCGTCAAA 9360
QY 9361 AGAGTCTTAATATATATATCCAGATGCGATGCTGTTACTTTATGTTACTACATGCACTTG 9420
Db 9361 AGAGTCTTAATATATATATCCAGATGCGATGCTGTTACTTTATGTTACTACATGCACTTG 9420
QY 9421 GCTGCATAAATGCTGATCAAGCATTTCTGTTGAAGGCGAGGTGCTTCAGGATACCATAT 9480
Db 9421 GCTGCATAAATGCTGATCAAGCATTTCTGTTGAAGGCGAGGTGCTTCAGGATACCATAT 9480
QY 9481 ACAGCTCAGAGTTTCTCTTTAGGCATTAATTTTAGCAAAATATCTCATCTCTCTTT 9540
Db 9481 ACAGCTCAGAGTTTCTCTTTAGGCATTAATTTTAGCAAAATATCTCATCTCTCTTT 9540
QY 9541 TTAACCATTTTCTTTTTTTTGTGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
Db 9541 TTAACCATTTTCTTTTTTTTGTGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT 9600
QY 9601 ACGTCAATGTAGAAAAGCTATAAATGAATACAATTAAGCTGTTATTTAAATAGCCAG 9660
Db 9601 ACGTCAATGTAGAAAAGCTATAAATGAATACAATTAAGCTGTTATTTAAATAGCCAG 9660
QY 9661 TGA AAAA ACTATTAACTGTTCTATTACCTGTTAGTATTATTTGTCATTA AAAATGCA 9720
Db 9661 TGA AAAA ACTATTAACTGTTCTATTACCTGTTAGTATTATTTGTCATTA AAAATGCA 9720
QY 9721 TATAC TTTTAAATGATATTGTTATGTATCTACTGCATGATTTTATTTAGAGTCTTGTC 9780
Db 9721 TATAC TTTTAAATGATATTGTTATGTATCTACTGCATGATTTTATTTAGAGTCTTGTC 9780
QY 9781 ATCTTGTATATACITAAATCGCTTTGTCATTTTGGAGACATTTATTTGCTTCTAATTT 9840
Db 9781 ATCTTGTATATACITAAATCGCTTTGTCATTTTGGAGACATTTATTTGCTTCTAATTT 9840
QY 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGGTAGCGGAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGTCTTACGGAATATTTTCAATCAACTGTGGTAGCGGAATTAATCGTGT 9900
QY 9901 TCTTCACTCAGGACATTTGCTCTAAGTGTGAAGACATTTGGTTATTTTACCAGCAAC 9960
Db 9901 TCTTCACTCAGGACATTTGCTCTAAGTGTGAAGACATTTGGTTATTTTACCAGCAAC 9960

Db 9901 TCTTCACTCAGGACATTTGCTCTAAGTGTGAAGACATTTGCTTATTTTACCAGCAAC 9960
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RESULT 8
US-08-834-497A-7
; Sequence 7, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnikke, Andreas
; APPLICANT: Ruddy, David

APPLICANT: Tsuchihashi, Zenta
 APPLICANT: Wolff, Roger K.
 TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/834,497A
 FILING DATE: 04-APR-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/652,265
 FILING DATE: 23-MAY-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/632,673
 FILING DATE: 16-APR-1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/630,912
 FILING DATE: 04-APR-1996
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Poissant, Brian M.
 REGISTRATION NUMBER: 28,462
 REFERENCE/DOCKET NUMBER: 8907-0056-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 7:
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 OTHER INFORMATION:
 OTHER INFORMATION: /label= 24d1
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: Patent No. 6228594
: GENERAL INFORMATION:
: APPLICANT: Thomas, Winston J.
: APPLICANT: Drayna, Dennis T.
: APPLICANT: Feder, John N.
: APPLICANT: Gnirke, Andreas
: APPLICANT: Ruddy, David
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Hereditary Hemochromatosis Gene
: NUMBER OF SEQUENCES: 44
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95
: SOFTWARE: WordPerfect Version 8
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/503,444A
: FILING DATE: 14-Feb-2000
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/652,265
: FILING DATE: 23-May-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/632,673
: FILING DATE: 16-Apr-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/630,912
: FILING DATE: 04-Apr-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 8907-0088-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-9741
: TELEX: 66141
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QY 2521 TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGACAGAAAGAGAATTTGG 2580
Db 2521 TATATTTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGACAGAAAGAGAATTTGG 2580
QY 2581 CTGGGTGTAGTAGTCTATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA 2640
Db 2581 CTGGGTGTAGTAGTCTATGCCAAGGAGGAGGCCAAGGAGAGCAGATTCCTGAGCTCAGGA 2640
QY 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
Db 2641 GTTCAAGACCAAGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGTGCATGCACCTGTGATCTCTAGTACTCGGGAGGCTGAGGTGAGGGA 2760
Db 2701 GCTGGGTGTGGTGCATGCACCTGTGATCTCTAGTACTCGGGAGGCTGAGGTGAGGGA 2760
QY 2761 TTGCTTGAGCCCAAGAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
Db 2761 TTGCTTGAGCCCAAGAGTTGAGGCTGCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
QY 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAGTTAAAGT 2880
Db 2821 CTAGGTGACAGCAAGACCCCTGTCTCCCTGACCCCTGAAAAAGAGAAGTTAAAGT 2880
QY 2881 TGACTTTGTTCTTTTATTTTAAATTTTATTGGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
Db 2881 TGACTTTGTTCTTTTATTTTAAATTTTATTGGCTGAGCAGTGGGTAATTTGGCAATGCCAT 2940
QY 2941 TTCTGAGATGTTGAAGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
Db 2941 TTCTGAGATGTTGAAGCAGAGGAAAGAGCAGTTTGGGGTAAATCAAGGATCTGCATTTG 3000
QY 3001 GGACATGTTAAGTTTGAATTTCCAGTTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3060
Db 3001 GGACATGTTAAGTTTGAATTTCCAGTTCAGGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3060
QY 3061 CAGTGTAAAGAAATTCAGGACCAAGCTGGGCACGGTGGCTCACTTCTGTAATCCAGCACT 3120
Db 3061 CAGTGTAAAGAAATTCAGGACCAAGCTGGGCACGGTGGCTCACTTCTGTAATCCAGCACT 3120
QY 3121 TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTGAGGAGTTTGACAGCAAGCTTGCCCAACA 3180
Db 3121 TTGGTGGCTGAGGCAGGTAGATCATTTGAGGTGAGGAGTTTGACAGCAAGCTTGCCCAACA 3180
QY 3181 TGGTGAACCCCATGTCTACTTAAATAACAAAAATAGCCCTGGTGGTGGCGCACGCCCT 3240
Db 3181 TGGTGAACCCCATGTCTACTTAAATAACAAAAATAGCCCTGGTGGTGGCGCACGCCCT 3240
QY 3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGTGCAGG 3300
Db 3241 ATAGTCCCAAGTTTTCAGGAGGCTTAGGTAGGAGAAATCCCTTGAAACCCAGGAGTGCAGG 3300
QY 3301 TTGCAGTGCAGTGAATGTGCCACTGCACCTCCAGCCCTGGGTGATAGAGTGCAGACTCTGT 3360
Db 3301 TTGCAGTGCAGTGAATGTGCCACTGCACCTCCAGCCCTGGGTGATAGAGTGCAGACTCTGT 3360
QY 3361 CTCAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3420
Db 3361 CTCAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3420
QY 3421 TCTAATTTGGCCCTGAGCACCACCTCTGAGTTCAACTTACCATGGCTGAGACACACCTTTAAC 3480
Db 3421 TCTAATTTGGCCCTGAGCACCACCTCTGAGTTCAACTTACCATGGCTGAGACACACCTTTAAC 3480
QY 3481 ATTTTCTAGATTCACCAAGCTTTTAGTGGAGTCTCTAATCATCAGTATTTGGATAGGAT 3540
Db 3481 ATTTTCTAGATTCACCAAGCTTTTAGTGGAGTCTCTAATCATGAGTATTTGGATAGGAT 3540
QY 3541 CTGGGGCAGTGGGGGTGGCAGCCACGCTGTGGCAGAGAAAGACACACAGGAAGAGC 3600
Db 3541 CTGGGGCAGTGGGGGTGGCAGCCACGCTGTGGCAGAGAAAGACACACAGGAAGAGC 3600

Db 5761 CCCAATGGGGATGGGACCTACCAGGCGTGGATAAACCTTGGGCTGTACCCCTCGGGGAAAGAG 5820
 QY 5821 CAGAGATATACGTTCCAGGTGGAGCACCCAGGCGCTGGATCAGCCCTCATTTGTGATCTGG 5880
 Db 5821 CAGAGATATACGTTGCCAGGTGGAGCACCCAGGCGCTGGATCAGCCCTCATTTGTGATCTGG 5880
 QY 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTAATGCGGGGTTGAGAGGAGTGCC 5940
 Db 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAAATCTAATGCGGGGTTGAGAGGAGTGCC 5940
 QY 5941 TGAGGAGGTAAATATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6000
 Db 5941 TGAGGAGGTAAATATGGCAGTGAGATGAGGATCTGCTCTTTGTTAGGGGGTGGGCTGAGG 6000
 QY 6001 GTGGCAATCAAAAGGCTTAACTTGTCTTTTCTGTTTATAGAGCCCTCAGCGTCTGGCAACC 6060
 Db 6001 GTGGCAATCAAAAGGCTTAACTTGTCTTTTCTGTTTATAGAGCCCTCAGCGTCTGGCAACC 6060
 QY 6061 TAGTCATTTGGAGTCACTAGTGGAAATGCTGTTTTTGTGCTCATCTTGTTTCATTTGGAATTT 6120
 Db 6061 TAGTCATTTGGAGTCACTAGTGGAAATGCTGTTTTTGTGCTCATCTTGTTTCATTTGGAATTT 6120
 QY 6121 TGTTCATATATTAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGAAAGTCTCT 6180
 Db 6121 TGTTCATATATTAAGGAAGAGCAGGGTTCAAGTGAGTAGGAACAAGGGGAAAGTCTCT 6180
 QY 6181 TAGTACCTCTGCCCGCAGGCGACAGTGGGAAGAGGGGACAGAGGGATCTGGCATCCATGGG 6240
 Db 6181 TAGTACCTCTGCCCGCAGGCGACAGTGGGAAGAGGGGACAGAGGGATCTGGCATCCATGGG 6240
 QY 6241 AAGCATTTTCTCATTTATATTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT 6300
 Db 6241 AAGCATTTTCTCATTTATATTTTGGGGACACAGCAGCTCCCTGGGAGACAGAAAT 6300
 QY 6301 AATGGTTCTCCCGCAGAAATGAAAGTCTAATCAACAACAATCTCAGAGCACCCTACTAT 6360
 Db 6301 AATGGTTCTCCCGCAGAAATGAAAGTCTAATCAACAACAATCTCAGAGCACCCTACTAT 6360
 QY 6361 TTTGCAAGAGCTCTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
 Db 6361 TTTGCAAGAGCTCTTAAAGTAGTACAGGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
 QY 6421 TCTCAGAACCCAAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTTAAGAAAG 6480
 Db 6421 TCTCAGAACCCAAATCTGTTAGGGAATGAAATTTGATAGCAAGTAAATGTTAAGAAAG 6480
 QY 6481 ACCCCATGAGTCTTAAGCAGCAGGAAGCAAAATCTTAAAGGTGTCAAGGAAAGAAATG 6540
 Db 6481 ACCCCATGAGTCTTAAGCAGCAGGAAGCAAAATCTTAAAGGTGTCAAGGAAAGAAATG 6540
 QY 6541 ATCACATTACGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA 6600
 Db 6541 ATCACATTACGCTGGGATCAAGATAGCCTTCTGGATCTTGAAGGAGAAGCTGGATTCCA 6600
 QY 6601 TTAGGTGAGTTGAAGATGATGGAGGTCTACACAGACGAGCAACCATGCCAAGTAGGA 6660
 Db 6601 TTAGGTGAGTTGAAGATGATGGAGGTCTACACAGACGAGCAACCATGCCAAGTAGGA 6660
 QY 6661 GAGTATAGGCATCTAGGGAGATTAGAAATAATTTACTGTACCTTAACCCCTGAGTTGGCT 6720
 Db 6661 GAGTATAGGCATCTAGGGAGATTAGAAATAATTTACTGTACCTTAACCCCTGAGTTGGCT 6720
 QY 6721 AGCTATCACTCACCAATATGCAATTTTACCCCTGAACATCTGTGGTGTAGGGAAGA 6780
 Db 6721 AGCTATCACTCACCAATATGCAATTTTACCCCTGAACATCTGTGGTGTAGGGAAGA 6780
 QY 6781 GAATCAGAAAAGACCCAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTTGGGTTATGA 6840
 Db 6781 GAATCAGAAAAGACCCAGCTCATACAGAGTCCAAAGGCTCTTTTGGGATATTTGGGTTATGA 6840
 QY 6841 TCACTGGGGTGTCTAATGAAGATCCCTAAGAAAGGAGGACCCAGCTCCCTTATATGGTG 6900
 Db 6841 TCACTGGGGTGTCTAATGAAGATCCCTAAGAAAGGAGGACCCAGCTCCCTTATATGGTG 6900

QY 6901 AATGTGTTGTTAAGAGTTAGATGAGAGGTGAGGAGACCAGTGTAGAAAGCCAATATAGCAT 6960
 Db 6901 AATGTGTTGTTAAGAGTTAGATGAGAGGTGAGGAGACCAGTGTAGAAAGCCAATATAGCAT 6960
 QY 6961 TTCAGATGAGAGATATGTTCTTTGAAATCCAAATAGTCCAGGCTCAAATTTGAGATGG 7020
 Db 6961 TTCAGATGAGAGATATGTTCTTTGAAATCCAAATAGTCCAGGCTCAAATTTGAGATGG 7020
 QY 7021 GTGAATGAGGAAAATAAGGAAGAGAGAGGCAAGATGTTGCTAGTCTAGTCTTGTGATGCT 7080
 Db 7021 GTGAATGAGGAAAATAAGGAAGAGAGAGGCAAGATGTTGCTAGTCTAGTCTTGTGATGCT 7080
 QY 7081 CTTTCTCGGCTCTCTGTCTCCACAGAGGAGCCATGGGCACTACGCTCTTACGTGAACG 7140
 Db 7081 CTTTCTCGGCTCTCTGTCTCCACAGAGGAGCCATGGGCACTACGCTCTTACGTGAACG 7140
 QY 7141 TGAGTGACACGCGCTGCAGACTCAGTCTGGGAAGAGACAAACTAGAGACTCAAAGA 7200
 Db 7141 TGAGTGACACGCGCTGCAGACTCAGTCTGGGAAGAGACAAACTAGAGACTCAAAGA 7200
 QY 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTTAAACATAGAAAT 7260
 Db 7201 GGGAGTGCATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGAACCTTAAACATAGAAAT 7260
 QY 7261 GCCTCAGCAACTCCTTGATTTAGCCTTCTGTTTCATTTCTCCCAAAAGATTTTCCCAT 7320
 Db 7261 GCCTCAGCAACTCCTTGATTTAGCCTTCTGTTTCATTTCTCCCAAAAGATTTTCCCAT 7320
 QY 7321 TTAGTTTCTGAGTCTCTGCGATGCCGCTGATCCCTAGCTGTGACCTCTCCCTGGAACTG 7380
 Db 7321 TTAGTTTCTGAGTCTCTGCGATGCCGCTGATCCCTAGCTGTGACCTCTCCCTGGAACTG 7380
 QY 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGCTTCTTCATTTTCTCCGTCACCTCAGAG 7440
 Db 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGCTTCTTCATTTTCTCCGTCACCTCAGAG 7440
 QY 7441 ACATACACCTATGTCATTTTCATTTTTCGGAAGAGACTTCTTAATTTTGGGGGA 7500
 Db 7441 ACATACACCTATGTCATTTTCATTTTTCGGAAGAGACTTCTTAATTTTGGGGGA 7500
 QY 7501 CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTCGGACGTGGCTAGTCAT 7560
 Db 7501 CTTACATGATTCATTTTAAACATCTGAGAAAAGCTTTGAACCTCGGACGTGGCTAGTCAT 7560
 QY 7561 AACCTTACAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTCAACCTTTTCT 7620
 Db 7561 AACCTTACAGATTTTACACATGATCTATGCAATTTTCTGGACCCGTTCAACCTTTTCT 7620
 QY 7621 TTGAATCCTCTCTGTGTTTACCAGTAACTCATCTGTCCACCAAGCCTTGGGGATTTCT 7680
 Db 7621 TTGAATCCTCTCTGTGTTTACCAGTAACTCATCTGTCCACCAAGCCTTGGGGATTTCT 7680
 QY 7681 CATCTGATGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
 Db 7681 CATCTGATGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCACGAATGGAAGAG 7740
 QY 7741 GCACCTGTCCAGAAAAAGCATCATGCTATCTGTGGGTAGTATGAGGGTGTGTTTTAGC 7800
 Db 7741 GCACCTGTCCAGAAAAAGCATCATGCTATCTGTGGGTAGTATGAGGGTGTGTTTTAGC 7800
 QY 7801 AGGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGCTTTTTTCTAATTTGGCATGA 7860
 Db 7801 AGGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGCTTTTTTCTAATTTGGCATGA 7860
 QY 7861 AGGTGTCTACAGATTTGCAAAAGTTTAAATGGTGGCTTCTCATTTGGGATCTACTCTAGTAT 7920
 Db 7861 AGGTGTCTACAGATTTGCAAAAGTTTAAATGGTGGCTTCTCATTTGGGATCTACTCTAGTAT 7920
 QY 7921 TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTGTTGATATGAAA 7980
 Db 7921 TCCAGACCTGAAGAATCACAATAATTTTCTACCTGGTCTCTCCTTGTGTTGATATGAAA 7980

Qy	7981	ATTATGATAGGATGATAAAGCACATTACTTGTGTCGACCTCTTCTGAGCACCTTACTTA	8040
Db	7981	ATTATGATAGGATGATAAAGCACATTACTTGTGTCGACCTCTTCTGAGCACCTTACTTA	8040
Qy	8041	CATCATTACTGCATGCATCTCTCAATAAATCTATGATAGTAGTACTATTATCTCCCAT	8100
Db	8041	CATCATTACTGCATGCATCTCTCAATAAATCTATGATAGTAGTACTATTATCTCCCAT	8100
Qy	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCGCGGCACGGTGGCTCAGCCCTGTAATCCC	8160
Db	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCGCGGCACGGTGGCTCAGCCCTGTAATCCC	8160
Qy	8161	AGCACTTTGGAGGCCAAAGCGGGTGGATCAGAGTCAGAGATCGAGACCATCTGGC	8220
Db	8161	AGCACTTTGGAGGCCAAAGCGGGTGGATCAGAGTCAGAGATCGAGACCATCTGGC	8220
Qy	8221	TAACATGGTCAAAACCCCATCTCTTAATAAAATACAAAAAATTAGCTGGCGCTGTGGCAG	8280
Db	8221	TAACATGGTCAAAACCCCATCTCTTAATAAAATACAAAAAATTAGCTGGCGCTGTGGCAG	8280
Qy	8281	ACGCCGTAGTCCACGCTACTCGGAAGGCTGAGGCAGGAGAAATGGCATGAACCCAGGAGG	8340
Db	8281	ACGCCGTAGTCCACGCTACTCGGAAGGCTGAGGCAGGAGAAATGGCATGAACCCAGGAGG	8340
Qy	8341	CAGAGCTTGCAGTGACCGGAGTTTGGCCOACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400
Db	8341	CAGAGCTTGCAGTGACCGGAGTTTGGCCOACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400
Qy	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA	8460
Db	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAA	8460
Qy	8461	TAGAGTATCTCATAGTTTGTGCTGATGATAAAACAGAGTTTCAAACCTCAGCTCAATCTGACCG	8520
Db	8461	TAGAGTATCTCATAGTTTGTGCTGATGATAAAACAGAGTTTCAAACCTCAGCTCAATCTGACCG	8520
Qy	8521	TTTGTATACATCTCAGACACACCTACATTCAGTAGTATTTAGATGCCCTAGAAATAAATAGAAA	8580
Db	8521	TTTGTATACATCTCAGACACACCTACATTCAGTAGTATTTAGATGCCCTAGAAATAAATAGAAA	8580
Qy	8581	GGAGGAGATGGCTCTTCTTGTCTCATGTGTGTTCTTCTGAGTGAGCTTGAATCACAT	8640
Db	8581	GGAGGAGATGGCTCTTCTTGTCTCATGTGTGTTCTTCTGAGTGAGCTTGAATCACAT	8640
Qy	8641	GAAGGGGAACAGCAGAGAAAACCAACTGATCCTCAGCTGTCATGTTTCCCTTAAAAAGTC	8700
Db	8641	GAAGGGGAACAGCAGAGAAAACCAACTGATCCTCAGCTGTCATGTTTCCCTTAAAAAGTC	8700
Qy	8701	CCCTGAAGGAAGTCTTGGAATGTGACTCCCTGCTCCTCTGTGTGCTCTCTTTTGGCATTTCA	8760
Db	8701	CCCTGAAGGAAGTCTTGGAATGTGACTCCCTGCTCCTCTGTGTGCTCTCTTTTGGCATTTCA	8760
Qy	8761	TTTCTTTGGACCTACGCAAGGACTGTAAATGGTGGGACAGCTAGTGGCCCTCTGCTGGC	8820
Db	8761	TTTCTTTGGACCTACGCAAGGACTGTAAATGGTGGGACAGCTAGTGGCCCTCTGCTGGC	8820
Qy	8821	TTCACACAGGTGTCTCCCTAGGCCAGTGCCTCTGAGTGCAGAACTCTGGTGGTATTTC	8880
Db	8821	TTCACACAGGTGTCTCCCTAGGCCAGTGCCTCTGAGTGCAGAACTCTGGTGGTATTTC	8880
Qy	8881	CCCTAATGAAGTGGATAGCTCTCTCATTTTGGAAATGGTATATGGAAGCCCAAGT	8940
Db	8881	CCCTAATGAAGTGGATAGCTCTCTCATTTTGGAAATGGTATATGGAAGCCCAAGT	8940
Qy	8941	GCCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCGGTGCACATTTAAAAA	9000
Db	8941	GCCTTAGAGATGCCAGGTCCTTCCATGGAGCCACTGGGTTCCGGTGCACATTTAAAAA	9000
Qy	9001	AAAATCTAACCCGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTTACCATTGTTC	9060
Db	9001	AAAATCTAACCCGACATTCAGGAATTGCTAGATTCTGGGAAATCAGTTTACCATTGTTC	9060
Qy	9061	AAAGAGTCTTTTTTTTTTTTTTTTTTTTGAGACTCTATTGCCCCAGGCTGGAGTGCATGAT	9120

Db	9061	AAAGAGTCTTTTTTTTTTTTTTTTTTTTTTTTGAGACTCTATTGCCCAGGCTGGAGTGCAATGSCATGAT	9120
Qy	9121	CTCGGCTCACATGTAACCTCTCCCTCCAGGTTCAAGGATTCCTCCTCTCAGCCTCCCA	9180
Db	9121	CTCGGCTCACATGTAACCTCTCCCTCCAGGTTCAAGGATTCCTCCTCTCAGCCTCCCA	9180
Qy	9181	AGTAGCTGGGATTACAGGCGTGCACCACCATGCGCGCTAAATTTTCTATTATTTTAGTAGA	9240
Db	9181	AGTAGCTGGGATTACAGGCGTGCACCACCATGCGCGCTAAATTTTCTATTATTTTAGTAGA	9240
Qy	9241	GACAGGGTTTCACCATGTTGGCCAGGCTGCTCGAACTCTCCTGACCTCGTGATCGGCC	9300
Db	9241	GACAGGGTTTCACCATGTTGGCCAGGCTGCTCGAACTCTCCTGACCTCGTGATCGGCC	9300
Qy	9301	TGCCTCGGCTCCCAAGATGCTGAGATACAGGTGTGAGCCACCCCTGCCAGCGCTCAAA	9360
Db	9301	TGCCTCGGCTCCCAAGATGCTGAGATACAGGTGTGAGCCACCCCTGCCAGCGCTCAAA	9360
Qy	9361	AGAGTCTTAATATATATATCCAGATGCGATGTGTTTACTTTATGTTACTACATGCACTTG	9420
Db	9361	AGAGTCTTAATATATATATCCAGATGCGATGTGTTTACTTTATGTTACTACATGCACTTG	9420
Qy	9421	GCTGCATAAATGTGGTACAAGCATCTCTTTGAAGGCGAGGTGCTTCAGGATACCATAT	9480
Db	9421	GCTGCATAAATGTGGTACAAGCATCTCTTTGAAGGCGAGGTGCTTCAGGATACCATAT	9480
Qy	9481	ACAGCTCAGAAGTTTCCTTTTAGGCATTAATAATTTAGCAAAAGATATCTCATCTCTCTT	9540
Db	9481	ACAGCTCAGAAGTTTCCTTTTAGGCATTAATAATTTAGCAAAAGATATCTCATCTCTCTT	9540
Qy	9541	TTAAACCATTTCTTTTTTGTGTGTAGAAAGTTATGTAGAAAAAGTAAATCTGATTT	9600
Db	9541	TTAAACCATTTCTTTTTTGTGTGTAGAAAGTTATGTAGAAAAAGTAAATCTGATTT	9600
Qy	9601	ACGCTCATTTGAGAAAAAGCTATAAAATGAATACAAATTTAAAGCTGTTATTTAAATTAGCCAG	9660
Db	9601	ACGCTCATTTGAGAAAAAGCTATAAAATGAATACAAATTTAAAGCTGTTATTTAAATTAGCCAG	9660
Qy	9661	TGAAAACTATTACAACTTGCTATTACCTGTTAGTATTATTGTTGTCATTAAAAATGCA	9720
Db	9661	TGAAAACTATTACAACTTGCTATTACCTGTTAGTATTATTGTTGTCATTAAAAATGCA	9720
Qy	9721	TATACTTTAATAAATGTATTGTATTGTATCTATGCAATGATTTATTGAAGTGTCTGTTC	9780
Db	9721	TATACTTTAATAAATGTATTGTATTGTATCTATGCAATGATTTATTGAAGTGTCTGTTC	9780
Qy	9781	ATCTTGATATATCTTAATCGCTTGTGCATTTTGGAGACATTTATTTCGCTCTAATTT	9840
Db	9781	ATCTTGATATATCTTAATCGCTTGTGCATTTTGGAGACATTTATTTCGCTCTAATTT	9840
Qy	9841	CTTTACATTTTGTCTTACGGAAATATTTTCATCACTGTGTTAGCGGAATTAATCTGTGT	9900
Db	9841	CTTTACATTTTGTCTTACGGAAATATTTTCATCACTGTGTTAGCGGAATTAATCTGTGT	9900
Qy	9901	TCCTTCACTCTAGGACATTTGCGTCTAAGTTGTAAAGACATTTGTTATTTTACCAGCAAC	9960
Db	9901	TCCTTCACTCTAGGACATTTGCGTCTAAGTTGTAAAGACATTTGTTATTTTACCAGCAAC	9960
Qy	9961	CATTCTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTACTATCTGAAAGCAGA	10020
Db	9961	CATTCTGAAAGCATATGACAAATTTTCTCTCTTAATATCTTACTACTATCTGAAAGCAGA	10020
Qy	10021	CTGCTATAAGGCTTCACTTACTCTTACCTCATAGGAATATGTTACAATTAATTTATT	10080
Db	10021	CTGCTATAAGGCTTCACTTACTCTTACCTCATAGGAATATGTTACAATTAATTTATT	10080
Qy	10081	AGGTAAGCATTTGTTTATATATGTTTTTATTTCACCTGGGCTCAGATTTCAAGAAACACC	10140
Db	10081	AGGTAAGCATTTGTTTATATGTTTTTATTTCACCTGGGCTCAGATTTCAAGAAACACC	10140
Qy	10141	CCAGTCTTCAAGTAAACACATTTTCACTTAACACATTTTACTAAACATCAGCAACTGTGSCCT	10200

bb 61 AATATCTAAGTTTCAGATCAGAACATTCGGAAGCTACTTTCCCAATCAACAACCCCT 120
QY 121 TCAGGATTTAAACCAAGGGGACACTGGATCACCCTAGTGTTCACAAAGCAGGTACCTT 180
Db 121 TCAGGATTTAAACCAAGGGGACACTGGATCACCCTAGTGTTCACAAAGCAGGTACCTT 180
QY 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTCTGAAAGACCTGTGCTTTTCACCAAGAACTT 240
Db 181 CTGCTGTAGGAGAGAGAACTAAAGTTCTGAAAGACCTGTGCTTTTCACCAAGAACTT 240
QY 241 TTACTTGGGATCTCTGAGCCTTAGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 300
Db 241 TTACTTGGGATCTCTGAGCCTTAGCAATAGCTGTAGGGTGACTTCTGGAGCCATCCCG 300
QY 301 TTTCCCGCCCGCCAAAAGAGCGAGATTTAAGCGGACCTGCGGCCAGAGCTGGGAA 360
Db 301 TTTCCCGCCCGCCAAAAGAGCGAGATTTAAGCGGACCTGCGGCCAGAGCTGGGAA 360
QY 361 ATGGCCCGCGAGCGAGCCCGGCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCTG 420
Db 361 ATGGCCCGCGAGCGAGCCCGGCTTCTCCTCTGATGCTTTTGCAGACCGCGGTCTG 420
QY 421 CAGGGCGCTTGTGCTGTAGTCGAGGCGTCCGCGGGAACCTAGGGCGCGGCGGGGTG 480
Db 421 CAGGGCGCTTGTGCTGTAGTCGAGGCGTCCGCGGGAACCTAGGGCGCGGCGGGGTG 480
QY 481 GAAAAATCGAACTAGCTTTTTCGCTTGGCTTGGAGTTTTCCTAACCTTTGGAGACCTGC 540
Db 481 GAAAAATCGAACTAGCTTTTTCGCTTGGAGTTTTCCTAACCTTTGGAGACCTGC 540
QY 541 TCAACCCCTATCCGAAGCCCTCTCCCTACTTCTTGGCTCGAGACCCCGCTGAGGGAGTGC 600
Db 541 TCAACCCCTATCCGAAGCCCTCTCCCTACTTCTTGGCTCGAGACCCCGCTGAGGGAGTGC 600
QY 601 CTACCAGTGAAGTGCAGATAGGGTCCCTCGCCCCAGAGCTGCCCCCTCCCCCGGCTGT 660
Db 601 CTACCAGTGAAGTGCAGATAGGGTCCCTCGCCCCAGAGCTGCCCCCTCCCCCGGCTGT 660
QY 661 CCCGCTCTCGGGAGTGACTTTTGGAAACCGCCACTCCCTTCCCCCACTAGATGCTTT 720
Db 661 CCCGCTCTCGGGAGTGACTTTTGGAAACCGCCACTCCCTTCCCCCACTAGATGCTTT 720
QY 721 TAAATAAATCTCGTAGTCTCACTTCTGAGCTGAGCTAAGCCTGGGCTCCTTGAACCTGG 780
Db 721 TAAATAAATCTCGTAGTCTCACTTCTGAGCTGAGCTAAGCCTGGGCTCCTTGAACCTGG 780
QY 781 AACTCGSGTTTATTTCCAAATGTCAGCTGTGAGTTTTCGCCAGTCATCTCCAAACAGG 840
Db 781 AACTCGSGTTTATTTCCAAATGTCAGCTGTGAGTTTTCGCCAGTCATCTCCAAACAGG 840
QY 841 AAGTTCTTCCCTGAGTGTGCGGAGAAAGCTGAGCAAAACCCACAGCAGATCCGCACCG 900
Db 841 AAGTTCTTCCCTGAGTGTGCGGAGAAAGCTGAGCAAAACCCACAGCAGATCCGCACCG 900
QY 901 GGTTCACCTCTAGAACGAATGCTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGA 960
Db 901 GGTTCACCTCTAGAACGAATGCTTGGGCGGTGGGGCGGAAAGAGTGGCGTTGGGA 960
QY 961 TCTGAATCTCTACCATTTCAACCCACTTTTGGTGAGACCTGGGGTGAGGTCFCTAGGTT 1020
Db 961 TCTGAATCTCTACCATTTCAACCCACTTTTGGTGAGACCTGGGGTGAGGTCFCTAGGTT 1020
QY 1021 GGGAGGCTCCTGAGAGAGGCTACCTCGGGCTTTCGCCACTCTTGGCAATGTTCTTTT 1080
Db 1021 GGGAGGCTCCTGAGAGAGGCTACCTCGGGCTTTCGCCACTCTTGGCAATGTTCTTTT 1080
QY 1081 GCCTGGAAAAATTAAGTATATGTTAGTCTTGAACGTTTGAACGAACAAATCTCTTTTCG 1140
Db 1081 GCCTGGAAAAATTAAGTATATGTTAGTCTTGAACGTTTGAACGAACAAATCTCTTTTCG 1140
QY 1141 CTAGGCTTTATGATTTGCAATGTGCTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200
Db 1141 CTAGGCTTTATGATTTGCAATGTGCTGTAATTAAGAGGCTCTCTCAAAAGTACTGA 1200

QY 1201 TAATGAACATGTAAAGCAATCACTCACTTCTAAGTTTACATTCATATCTGATCTTATTGA 1260
Db 1201 TAATGAACATGTAAAGCAATCACTCACTTCTAAGTTTACATTCATATCTGATCTTATTGA 1260
QY 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATAAGCTTTATTTTACTAGAAGTTAACT 1320
Db 1261 TTTTCACTAGGCATAGGAGGTAGGAGCTAAATAAGCTTTATTTTACTAGAAGTTAACT 1320
QY 1321 GGAATTCAGATTTATAAATCTTTTTCAGGTTTACAAAGAACATAAATAAATCTGGTTCTG 1380
Db 1321 GGAATTCAGATTTATAAATCTTTTTCAGGTTTACAAAGAACATAAATAAATCTGGTTCTG 1380
QY 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAAATCTTAACTTGTGACAGTGAATTTGCCCTGTAG 1440
Db 1381 ATGTTATTTCAAGTACTACAGCTGCTTCTAAATCTTAACTTGTGACAGTGAATTTGCCCTGTAG 1440
QY 1441 TGTAGCACAGTGTCTGTGGGTACACGGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
Db 1441 TGTAGCACAGTGTCTGTGGGTACACGGCGGCTCAGCACAGCAGCTTTGAGTTTGGTA 1500
QY 1501 CTACGTTATCCACATTTTACACATGACAAGATGAGGATGGCAGCGCTGCTTCCCTCG 1560
Db 1501 CTACGTTATCCACATTTTACACATGACAAGATGAGGATGGCAGCGCTGCTTCCCTCG 1560
QY 1561 CAAATTTTCAATGTACAGTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
Db 1561 CAAATTTTCAATGTACAGTGGGCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGC 1620
QY 1621 TATGATCTTAAACATCAGCTGCATTTAGAGTTGAATTAATAAATTTTCAATGTGAGCAG 1680
Db 1621 TATGATCTTAAACATCAGCTGCATTTAGAGTTGAATTAATAAATTTTCAATGTGAGCAG 1680
QY 1681 AAATATTCATTTGTTTACAAAGTGTAAATGAGTCCAGCCATGTTGTCAGCTGTTCAAGCC 1740
Db 1681 AAATATTCATTTGTTTACAAAGTGTAAATGAGTCCAGCCATGTTGTCAGCTGTTCAAGCC 1740
QY 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGAGA 1800
Db 1741 CAAGGAGAGAGCAGGGAACAAAGTCTTTACCCCTTTGATATTTTGCATTTCTAGTGGAGA 1800
QY 1801 GATGACAATTAAGCAATAGCAGAAAGATATACACATCAGAAATCATGGTGTGTGTA 1860
Db 1801 GATGACAATTAAGCAATAGCAGAAAGATATACACATCAGAAATCATGGTGTGTGTA 1860
QY 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAAGCAGAGACATGAAGA 1920
Db 1861 GAAGCAGAGAAGTCAAGGCAAGTCACTCTGGGCTGACACTTGAAGCAGAGACATGAAGA 1920
QY 1921 AATAAGAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
Db 1921 AATAAGAATGATTTGACTGGGAGCAGTATTTCCAGGCAAACTGAGTGGGCTGGCAAG 1980
QY 1981 TTTGGATTTAAAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
Db 1981 TTTGGATTTAAAAACGGGTTTTCTCAGCACTACTCATGTGTGTGTGTGGGGGGGGGG 2040
QY 2041 CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCATGTAGGATGCTAGCAGTATCCTGT 2100
Db 2041 CGGCGTGGGGTGGGAAGGGGACTTACCATCTGCATGTAGGATGCTAGCAGTATCCTGT 2100
QY 2101 CTTCCCTACTCTACTAGTGTAGGAGCAGTCCGCCAGTCTTGGACAACCAAAATGCTCT 2160
Db 2101 CTTCCCTACTCTACTAGTGTAGGAGCAGTCCGCCAGTCTTGGACAACCAAAATGCTCT 2160
QY 2161 AAACCTTTCACATCTCAGCTAGTAGACAAACTCTCTGTTTAAAGAGCTCGGGTTGAAAA 2220
Db 2161 AAACCTTTCACATCTCAGCTAGTAGACAAACTCTCTGTTTAAAGAGCTCGGGTTGAAAA 2220
QY 2221 AATAACAAGTAGTCTCTGGGAGTAGAGGCCAAGAGTAGTAAATGGCTCAGAGAGGA 2280
Db 2221 AATAACAAGTAGTCTCTGGGAGTAGAGGCCAAGAGTAGTAAATGGCTCAGAGAGGA 2280

QY 2281 GCCACAAACAAGTTCTGCAGGCGCTGTAGGCTGTGTGTAATTTCTAGCCAAAGGAGTA 2340
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Db 2281 GCCACAAACAAGTTCTGCAGGCGCTGTAGGCTGTGTGTAATTTCTAGCCAAAGGAGTA 2340
QY 2341 ACAGTGTATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAAGCAGAATG 2400
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Db 2341 ACAGTGTATCTGTACAGGCTTTTAAAGATTTGCTCTGGCTGTATGTGGAAAGCAGAATG 2400
QY 2401 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAAGCTGTTACACAGTCCAGGCAG 2460
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Db 2401 AAGGGAGCAACAGTAAAGCAGGGAGCCAGCCAGGAAAGCTGTTACACAGTCCAGGCAG 2460
QY 2461 AGGTAGTGGAGTGGCTGGTGGGAACAGAAAGAGGAGTGACAAACCAATTTCTCTCTGAA 2520
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Db 2461 AGGTAGTGGAGTGGCTGGTGGGAACAGAAAGAGGAGTGACAAACCAATTTCTCTCTGAA 2520
QY 2521 TATATTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG 2580
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Db 2521 TATATTCTGAAGGAAGTTGCTGAAGGATTTCTATGTTGTGTGAGAGAAAGAGAATTTGG 2580
QY 2581 CTGGGTGTAGTCAATGCCAAGGAGGAGGCCAAGSAGAGCAGATTTCTGTAGCTCAGGA 2640
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Db 2581 CTGGGTGTAGTCAATGCCAAGGAGGAGGCCAAGSAGAGCAGATTTCTGTAGCTCAGGA 2640
QY 2641 GTTCAAGACCAGGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
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Db 2641 GTTCAAGACCAGGCTGGGCAACACAGCAAAACCCCTTCTCTACAAAAATACAAAAATTA 2700
QY 2701 GCTGGGTGTGGTCATGCATGCCAAGGAGGAGGCCAAGSAGAGCAGATTTCTGTAGCTCAGGA 2760
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Db 2701 GCTGGGTGTGGTCATGCATGCCAAGGAGGAGGCCAAGSAGAGCAGATTTCTGTAGCTCAGGA 2760
QY 2761 TTGCTTGAGCCCAAGAAAGTTGAGGCTCAGTGAGCCATGACTGTGCCACTGTACTTCAGC 2820
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QY 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAGAGAGAGTTTAAAGT 2880
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Db 2821 CTAGGTGACAGAGCAAGCCCTGTCTCCCTGACCCCTGAAAAGAGAGAGTTTAAAGT 2880
QY 2881 TGACTTTGTTCTTTATTTTAAATTTTATTGGCTGAGCAGTGGGGTAAATGGCAATGCCAT 2940
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Db 2881 TGACTTTGTTCTTTATTTTAAATTTTATTGGCTGAGCAGTGGGGTAAATGGCAATGCCAT 2940
QY 2941 TTCTGAGATGGTGAAGGCAGAGAAAGCAGTGTGGGTAAATCAAGAGATCTGCATTTG 3000
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Db 2941 TTCTGAGATGGTGAAGGCAGAGAAAGCAGTGTGGGTAAATCAAGAGATCTGCATTTG 3000
QY 3001 GGACATGTTAAGTTTGAGATTCAGTCAAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3060
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Db 3001 GGACATGTTAAGTTTGAGATTCAGTCAAGCTTCCAAGTGGTGAGGCCACATAGGCAGTT 3060
QY 3061 CAGTGTAGAATTCAGGACCAAGGCTGGGACGGTGGCTCAGTCTCTGTAATCCAGCAGCT 3120
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Db 3061 CAGTGTAGAATTCAGGACCAAGGCTGGGACGGTGGCTCAGTCTCTGTAATCCAGCAGCT 3120
QY 3121 TTGTGGCTGAGGCAGGTFAGATCATTTGAGTCAAGAGTTTGAGACAAGCTTGGCCAAACA 3180
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Db 3121 TTGTGGCTGAGGCAGGTFAGATCATTTGAGTCAAGAGTTTGAGACAAGCTTGGCCAAACA 3180
QY 3181 TGGTGAACCCCATCTCTACTTAAATAACAAAAATTTAGCCCTGGTGTGGTGGCGACGCCT 3240
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Db 3181 TGGTGAACCCCATCTCTACTTAAATAACAAAAATTTAGCCCTGGTGTGGTGGCGACGCCT 3240
QY 3241 ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGGAGATCCCTTTGAACCCAGGAGTGCAGG 3300
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Db 3241 ATAGTCCAGGTTTTTCAGGAGGCTTAGGTAGGAGATCCCTTTGAACCCAGGAGTGCAGG 3300
QY 3301 TTGCGAGTGAGCTGAGATTTGGCCACTGCACATCCAGCCCTGGGTGATAGAGTGAGACTCTGT 3360
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Db 3301 TTGCGAGTGAGCTGAGATTTGGCCACTGCACATCCAGCCCTGGGTGATAGAGTGAGACTCTGT 3360
QY 3361 CTCAAAAAAGGACGTGCCCTGCACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 4500
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Db 3361 CTCAAAAAAGGACGTGCCCTGCACAGCTGCAGAGTAAAGGAATTTATTCCTCAGGATTTGGG 3420
QY 3421 TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATTGCTAGACACACCTTTAAC 3480
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Db 3421 TCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAACTACCATTGCTAGACACACCTTTAAC 3480
QY 3481 ATTTTCTAGAATCCACCAGCTTTTAGTGGAGTCTGCTAATAATCATGAGTATTTGGAATAGAT 3540
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Db 3481 ATTTTCTAGAATCCACCAGCTTTTAGTGGAGTCTGCTAATAATCATGAGTATTTGGAATAGAT 3540
QY 3541 CTGGGGCAGTGAAGGGGTGCGACGCCAGCTGTGCGACAGAAAAGCACACAGGAAAGAGC 3600
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Db 3541 CTGGGGCAGTGAAGGGGTGCGACGCCAGCTGTGCGACAGAAAAGCACACAGGAAAGAGC 3600
QY 3601 ACCCAGGACTGTCATATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA 3660
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Db 3601 ACCCAGGACTGTCATATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAAATGAGGA 3660
QY 3661 CCAGACACAGCTGATGATGATGAGTTGATGAGGTGTGTGGAGCCTCAACATCCTGCTCCC 3720
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Db 3661 CCAGACACAGCTGATGATGATGAGTTGATGAGGTGTGTGGAGCCTCAACATCCTGCTCCC 3720
QY 3721 CTCCTACTACACATGTTAAGSCCTGTTGCTCTGCTCCAGGTTTCACACTCTCTGCACACTA 3780
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Db 3721 CTCCTACTACACATGTTAAGSCCTGTTGCTCTGCTCCAGGTTTCACACTCTCTGCACACTA 3780
QY 3781 CCTCTTCATGSGTGCTCAGACGAGACCTTTGGTCTTTTCCTTTGTTGAGCTTTGGGCTA 3840
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Db 3781 CCTCTTCATGSGTGCTCAGACGAGACCTTTGGTCTTTTCCTTTGTTGAGCTTTGGGCTA 3840
QY 3841 CGTGATGACACAGCTGTTGCTGTTCTATGATNATGAGAGTCCCGTGTGGAGCCCGGAAC 3900
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Db 3841 CGTGATGACACAGCTGTTGCTGTTCTATGATCATGAGAGTCCCGTGTGGAGCCCGGAAC 3900
QY 3901 TCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGAGTCTGAA 3960
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Db 3901 TCCATGGGTTTTCCAGTAGAATTTCAAGCCAGATGTGGCTGCAGCTGAGTCAAGAGTCTGAA 3960
QY 3961 AGGGTGGGATCACATGTTTCACTGTTGACTTCCTGAGGTGTGTCAGAGCTTTTCATCTTTTC 4020
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Db 3961 AGGGTGGGATCACATGTTTCACTGTTGACTTCCTGAGGTGTGTCAGAGCTTTTCATCTTTTC 4020
QY 4021 CAAGGTATGTGAGAGGGGGCTCACCCTCCTGAGGTGTGTCAGAGCTTTTCATCTTTTC 4080
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Db 4021 CAAGGTATGTGAGAGGGGGCTCACCCTCCTGAGGTGTGTCAGAGCTTTTCATCTTTTC 4080
QY 4081 ATGCATCTTTGAAGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAGAGGAAG 4140
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Db 4081 ATGCATCTTTGAAGAAACAGCTGGAAGTCTGAGGTCTTGTGGGAGCAGGAAGAGGAAG 4140
QY 4141 GAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGGTGGAAATAGGACCTATTCTTT 4200
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Db 4141 GAATTTGCTTCTGAGATCATTTTGGTCTTGGGATGGTGGAAATAGGACCTATTCTTT 4200
QY 4201 TGGTTTCAGTTTAAAGGCTGGGGATTTTTCAGAGTCCACACCCCTGCAGGTCACTCTG 4260
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Db 4201 TGGTTTCAGTTTAAAGGCTGGGGATTTTTCAGAGTCCACACCCCTGCAGGTCACTCTG 4260
QY 4261 GGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
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Db 4261 GGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG 4320
QY 4321 CAGGACCACTTCAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAAACCCAGGGCC 4380
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Db 4321 CAGGACCACTTCAATTTCTGCCCTGACACACTGGATTGGAGAGCAGCAAAACCCAGGGCC 4380
QY 4381 TGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTGGGCCAGGCAAGAGGCGCTAC 4440
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Db 4381 TGGCCCAACCAAGCTGGAGTGGGAAAGGCACAAGATTTGGGCCAGGCAAGAGGCGCTAC 4440
QY 4441 CTGAGAGGAGCTGCCCTGCACAGCTGCAGAGTTGCTGGAGCTGGGGAGAGGTGTTTTG 4500
|||||

Db 4441 CTGGAGAGGGACTGCCCTGCACAGCTGCAGCAGTTGCTGGAGCTGGGAGAGGTGTTTG 4500
QY 4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG 4560
Db 4501 GACCAACAAGGTATGGTGGAAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG 4560
QY 4561 AGGTTGCAGGCGACGGAAATCCCTGGTTGGAGTTTCAGAGSTGGCTGAGGCTGTGTGCCCTC 4620
Db 4561 AGGTTGCAGGCGACGGAAATCCCTGGTTGGAGTTTCAGAGSTGGCTGAGGCTGTGTGCCCTC 4620
QY 4621 TCCAAATTTCTGGGAGGAGCACTTCTCAATCCTAGAGTCTCTACCTTATAATTTAGATGTGA 4680
Db 4621 TCCAAATTTCTGGGAGGAGCACTTCTCAATCCTAGAGTCTCTACCTTATAATTTAGATGTGA 4680
QY 4681 TGAGACAGCCACAAGTCAATGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
Db 4681 TGAGACAGCCACAAGTCAATGGTTTAAATTTCTTTCTCCATGCATATGGCTCAAAAGGAA 4740
QY 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
Db 4741 GTGCTATGGCCCTTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA 4800
QY 4801 AAATTCAGAAATGTCAAGCCGGCGGACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG 4860
Db 4801 AAATTCAGAAATGTCAAGCCGGCGGACGGTGGCTCACCCCTGTAATCCCAGCACTTTGGG 4860
QY 4861 AGGCCGAGCGGGTGTGCACAAAGTTCAGAGTTCAGAGTTCAGACCAAGCTGACCAACATGTTGAA 4920
Db 4861 AGGCCGAGCGGGTGTGCACAAAGTTCAGAGTTCAGAGTTCAGACCAAGCTGACCAACATGTTGAA 4920
QY 4921 ACCCGTCTCTAAAAAATFACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980
Db 4921 ACCCGTCTCTAAAAAATFACAAAAATTAGCTGGTCACAGTCATGCGCACCTGTAGTCCCA 4980
QY 4981 GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAGCGGAAGTTGCACTGA 5040
Db 4981 GCTAATTTGGAAGGCTGAGGCGAGGAGCATCGCTTGAACCTGGGAGCGGAAGTTGCACTGA 5040
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Db 5041 GCCAAGATCGGCCACTGCATCCAGCCTAGGCAGCAGAGTGAGACTCCATCTTAAAAAA 5100
QY 5101 AAAAAAATAAAGAGAAATTCAGAGATCTCAGTATCATATGAATACCAGGACAAA 5160
Db 5101 AAAAAAATAAAGAGAAATTCAGAGATCTCAGTATCATATGAATACCAGGACAAA 5160
QY 5161 ATATCAAGTGAAGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAGTTCCTTTTCAT 5220
Db 5161 ATATCAAGTGAAGCCACTTATCAGAGTAGAAGATCCTTTAGGTTAAAGTTCCTTTTCAT 5220
QY 5221 AGAATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCCGCTTCTTATAACAATGC 5280
Db 5221 AGAATAGCAATAATCACTGAAGCTACCTATCTTACAAGTCCCGCTTCTTATAACAATGC 5280
QY 5281 CTCCTAGTTGACCCAGGTGAAATGACCATCTGTATTTCAATCAATTTTCAATGCACATAA 5340
Db 5281 CTCCTAGTTGACCCAGGTGAAATGACCATCTGTATTTCAATCAATTTTCAATGCACATAA 5340
QY 5341 AGGCAATTTTATCTATCAGAACAAAGACATGGGTAAACATATGTATTTACATGTG 5400
Db 5341 AGGCAATTTTATCTATCAGAACAAAGACATGGGTAAACATATGTATTTACATGTG 5400
QY 5401 AGGAGAACAAAGCTGATCTGACTGTCTCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
Db 5401 AGGAGAACAAAGCTGATCTGACTGTCTCCAAGTGACACTGTGTTAGAGTCCCAATCTTAGG 5460
QY 5461 ACACAAAATGGTGTCTCTCCTGTAGCTGTTTTTTCTGAAAAAGGATTTTCTCTCTCCTC 5520
Db 5461 ACACAAAATGGTGTCTCTCCTGTAGCTGTTTTTTCTGAAAAAGGATTTTCTCTCTCCTC 5520
QY 5521 AACCTATAGAGGAGTCAAAAGTTCCAGTCTCTCTGCGCAAGGGTAAACATCCCCCTCTC 5580
Db 5521 AACCTATAGAGGAGTCAAAAGTTCCAGTCTCTCTGCGCAAGGGTAAACATCCCCCTCTC 5580

QY 5581 CTCATCCTTCTCTTCCCTCAAGTGCCTCCTTTTGGTGAAGTGACACATCATGTGACC 5640
Db 5581 CTCATCCTTCTCTTCCCTCAAGTGCCTCCTTTTGGTGAAGTGACACATCATGTGACC 5640
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Db 5641 TCTTCAGTGACCACTCTACGGTGTGCGGGCTTGAACCTACTACCCCCAGAACATCACCATTG 5700
QY 5701 AGTGGCTGAAGATTAAGCAGCAATGATGTCGAAGAGTTCGAACCTAAAGACGTATTG 5760
Db 5701 AGTGGCTGAAGATTAAGCAGCAATGATGTCGAAGAGTTCGAACCTAAAGACGTATTG 5760
QY 5761 CCCAATGGGATGGGACCTACCAAGGCTGTGATAACCTTGGCTGTACCCCTGGGAAGAG 5820
Db 5761 CCCAATGGGATGGGACCTACCAAGGCTGTGATAACCTTGGCTGTACCCCTGGGAAGAG 5820
QY 5821 CAGAGATATACGTCNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTATCTGG 5880
Db 5821 CAGAGATATACGTCNCCAGGTGGAGCACCCAGGCTGGATCAGCCCTCATTTGTATCTGG 5880
QY 5881 GGTATGTGACTGATGAGAGCCAGGAGCTGAGAAATCTATTGGGGTTGAGAGGAGTGCC 5940
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QY 5941 TGAGGAGGTAAATTTATGGCAGTGAGATGAGATCTGCTCTTTTGTAGGGGTGGGCTGAGG 6000
Db 5941 TGAGGAGGTAAATTTATGGCAGTGAGATGAGATCTGCTCTTTTGTAGGGGTGGGCTGAGG 6000
QY 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTGTAGAGCCCTCACCGTCTGGCACCC 6060
Db 6001 GTGGCAATCAAGGCTTTAACTTGTCTTTTGTAGAGCCCTCACCGTCTGGCACCC 6060
QY 6061 TAGTCATTTGGAGTCATCAGTGGAAATGCTTTTGTCTGCTCATCTTGTTCATTGGAATTT 6120
Db 6061 TAGTCATTTGGAGTCATCAGTGGAAATGCTTTTGTCTGCTCATCTTGTTCATTGGAATTT 6120
QY 6121 TGTTCATAATATTAAGAAAGAGCAGGTTCAAGTGAGTAGGAACAAGGGGAAGTCTCT 6180
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QY 6181 TAGTACCTTGCCCCAGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 6240
Db 6181 TAGTACCTTGCCCCAGGCACAGTGGGAAGAGGGGCAGAGGGGATCTGGCATCCATGGG 6240
QY 6241 AAGCATTTTCTCATTTATTTCTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAT 6300
Db 6241 AAGCATTTTCTCATTTATTTCTTTGGGACACCAAGCAGCTCCCTGGGAGACAGAAAT 6300
QY 6301 AATGGTCTCCCCAGAAATGAAAGTCTCTAATTCACAAAACATCTTCAGAGCACCTACTAT 6360
Db 6301 AATGGTCTCCCCAGAAATGAAAGTCTCTAATTCACAAAACATCTTCAGAGCACCTACTAT 6360
QY 6361 TTTGCAAGAGCTGTTTAAAGTAGTACAGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
Db 6361 TTTGCAAGAGCTGTTTAAAGTAGTACAGGGCTTTGAGGTTGAGAAGTCACTGTGGCTAT 6420
QY 6421 TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTAGTAGCAAGTAAATGTAGTTAAAGAG 6480
Db 6421 TCTCAGAACCCCAATCTGTTAGGGAATGAAATTTAGTAGCAAGTAAATGTAGTTAAAGAG 6480
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Db 6481 ACCCCATGAGGTCTTAAAGCAGGAGCAAGCAATGCTTTAGGGTGTCAAGGAAAAGATG 6540
QY 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA 6600
Db 6541 ATCACAATTCAGCTGGGGATCAAGATAGCCCTTCTGGATCTTGAAGGAGAGCTGGATTCCA 6600
QY 6601 TTAGGTGAGGTGAACATGATGGGAGGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660
Db 6601 TTAGGTGAGGTGAACATGATGGGAGGTCTACACAGCAGGAGCAACCATGCCAAGTAGGA 6660

QY	6661	GAGTATAGGGATAC	TCTGGGAGATTAGAAATAT	ACTGTACCTTAA	CCCTGAGTTCCGT	6720
DB	6661	GAGTATAGGCATAC	TCTGGGAGATTAGAAATAT	ACTGTACCTTAA	CCCTGAGTTCCGT	6720
QY	6721	AGCTATCACTACCA	ATTATGCAATTTCTAC	CCCTTGAACATCTGT	GTGTAGGGAAGA	6780
DB	6721	AGCTATCACTACCA	ATTATGCAATTTCTAC	CCCTTGAACATCTGT	GTGTAGGGAAGA	6780
QY	6781	GAATCAGAAAGACC	AGCTCATACAGAGTCCA	AGGGTCTTTTGGGATATT	GGGTATATGA	6840
DB	6781	GAATCAGAAAGACC	AGCTCATACAGAGTCCA	AGGGTCTTTTGGGATATT	GGGTATATGA	6840
QY	6841	TCAC	TGGGTCTCATTTGAAGGATCCTT	AGAAAGGAGGAC	CAGATCTCCCTTATATGGT	6900
DB	6841	TCAC	TGGGTCTCATTTGAAGGATCCTT	AGAAAGGAGGAC	CAGATCTCCCTTATATGGT	6900
QY	6901	AATGTGTTGTTA	GAAAGCTTAGATGAGAGTGAGG	AGACAGTATAGAAAGCCAA	TAAAGCATTAAGCAT	6960
DB	6901	AATGTGTTGTTA	GAAAGCTTAGATGAGAGTGAGG	AGACAGTATAGAAAGCCAA	TAAAGCATTAAGCAT	6960
QY	6961	TTCCAGATGAGAG	ATAATGGTCTTCAAATCCA	ATAGTGCCAGGTCFAAATTCAGATGG		7020
DB	6961	TTCCAGATGAGAG	ATAATGGTCTTCAAATCCA	ATAGTGCCAGGTCFAAATTCAGATGG		7020
QY	7021	GTGAATCAGGAA	ATAAGGAAGAGCAAGG	CAGATGGTGCCTTGGTATGCCT		7080
DB	7021	GTGAATCAGGAA	ATAAGGAAGAGCAAGG	CAGATGGTGCCTTGGTATGCCT		7080
QY	7081	CTTTCTCGGTCT	TTGTCTCCACAGGAGG	ACCATGGGACATACGCTTTAGCTGAACG		7140
DB	7081	CTTTCTCGGTCT	TTGTCTCCACAGGAGG	ACCATGGGACATACGCTTTAGCTGAACG		7140
QY	7141	TGAGTGACGCGC	CTCGAGCTACTCTGGG	AGGAGACAAACTAGACACTCAAGA		7200
DB	7141	TGAGTGACGCGC	CTCGAGCTACTCTGGG	AGGAGACAAACTAGACACTCAAGA		7200
QY	7201	GGGAGTGCAATTA	TGAGCTCTTCATGTTTC	CAGGAGAGTTGAACCTAAACATAGAAAT		7260
DB	7201	GGGAGTGCAATTA	TGAGCTCTTCATGTTTC	CAGGAGAGTTGAACCTAAACATAGAAAT		7260
QY	7261	GCCTGAGCACTCT	CTGATTTAGCCCTCTCTGTT	CATTCTCTCAAAAGATTTCCCAT		7320
DB	7261	GCCTGAGCACTCT	CTGATTTAGCCCTCTCTGTT	CATTCTCTCAAAAGATTTCCCAT		7320
QY	7321	TTAGGTTTCTG	AGTTCCTGCATCCCGGTGAT	CCCTAGCTGTGACCTCTCCCTGGAAC	CTG	7380
DB	7321	TTAGGTTTCTG	AGTTCCTGCATCCCGGTGAT	CCCTAGCTGTGACCTCTCCCTGGAAC	CTG	7380
QY	7381	TCTCTCATGA	ACCTCAAGCTGCATCTAG	AGGCTTCTTCAATTTCTCGTCA	CCCTCAG	7440
DB	7381	TCTCTCATGA	ACCTCAAGCTGCATCTAG	AGGCTTCTTCAATTTCTCGTCA	CCCTCAG	7440
QY	7441	ACATACACCTAT	GTCAATTCATTTCTATTTT	TGGAAGGACTCTTAAATTTGGGGGA		7500
DB	7441	ACATACACCTAT	GTCAATTCATTTCTATTTT	TGGAAGGACTCTTAAATTTGGGGGA		7500
QY	7501	CTTACATGATTC	ATTAAACATCTGAGAAAG	CTTTGAACCTGGGAGTGGGTAGTCAT		7560
DB	7501	CTTACATGATTC	ATTAAACATCTGAGAAAG	CTTTGAACCTGGGAGTGGGTAGTCAT		7560
QY	7561	AACCTTAC	CAGATTTTACACATGTATCT	ATCATTTTCTGGACCGGTCAACCTTTCC		7620
DB	7561	AACCTTAC	CAGATTTTACACATGTATCT	ATCATTTTCTGGACCGGTCAACCTTTCC		7620
QY	7621	TTGAATCCTCT	CTGTGTGTACCCAGTA	ACTCATCTGTCA	CCAGCCCTGGGATCTTC	7680
DB	7621	TTGAATCCTCT	CTGTGTGTACCCAGTA	ACTCATCTGTCA	CCAGCCCTGGGATCTTC	7680
QY	7681	CATCTGATTTG	TGATGAGTTGCAGCTAT	GAAAGCTGTACACTGC	ACGATGGAGAG	7740
DB	7681	CATCTGATTTG	TGATGAGTTGCAGCTAT	GAAAGCTGTACACTGC	ACGATGGAGAG	7740
QY	7741	GCACCTCTCC	CAGAAAGCATCATGGCT	TATCTGTGGGTAGTATGATGGGT	TGTTTTAGC	7800

Db	7741		GCACCTTCCAGAAAAGCATCATGGCTATCTGTGGTAGTATGATGGGTGTTTTAGC	7800
Qy	7801	AGGTAGGAGCAAAATATCTTTGAAGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA	7850	
Db	7801	AGGTAGGAGCAAAATATCTTTGAAGGGTGTGAAGAGGTGTTTTTCTTAATTTGGCATGA	7860	
Qy	7861	AGGTGTCATACAGATTTGGCAAGTTTAATGTGGCCCTCAATTTGGGATGCTACTCTAGTAT	7920	
Db	7861	AGGTGTCATACAGATTTGGCAAGTTTAATGTGGCCCTCAATTTGGGATGCTACTCTAGTAT	7920	
Qy	7921	TCCAGACCTGAAGAATCACAAATAATTTTCTACTGTGCTCTCCTTGTTCATGAAATGA	7980	
Db	7921	TCCAGACCTGAAGAATCACAAATAATTTTCTACTGTGCTCTCCTTGTTCATGAAATGA	7980	
Qy	7981	ATTATGATAAGGATGATAAAGCACCTTACTTCGTGTCGACCTTCTTGAGCACCTACTT	8040	
Db	7981	ATTATGATAAGGATGATAAAGCACCTTACTTCGTGTCGACCTTCTTGAGCACCTACTT	8040	
Qy	8041	CATGCATTACTGCATGCACCTCTTACAAATAATTCATGAGATAGTACTAATATCCCAT	8100	
Db	8041	CATGCATTACTGCATGCACCTCTTACAAATAATTCATGAGATAGTACTAATATCCCAT	8100	
Qy	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCGGGCACGGTGGCTCAGCCCTGTAATCCC	8160	
Db	8101	TTCTTTTTTAAATGAAGAAAGTGAAGTAGCGGGCACGGTGGCTCAGCCCTGTAATCCC	8160	
Qy	8161	AGCACTTTGGAGGCCAAACGGGTGGATCAGAGGTACAGAGATCGAGACCATCTGTGC	8220	
Db	8161	AGCACTTTGGAGGCCAAACGGGTGGATCAGAGGTACAGAGATCGAGACCATCTGTGC	8220	
Qy	8221	TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTTAGCTGGCGCTGTGTGGCAG	8280	
Db	8221	TAACATGGTGAACCCCATCTCTAATAAAAAATACAAAAATTTAGCTGGCGCTGTGTGGCAG	8280	
Qy	8281	ACGCCCTGTAGTCCCACTACTCGGAAGGTGAGGCAGAGAAATGGCATGAACCCAGGAGG	8340	
Db	8281	ACGCCCTGTAGTCCCACTACTCGGAAGGTGAGGCAGAGAAATGGCATGAACCCAGGAGG	8340	
Qy	8341	CAGAGCTTGCACTGAGCGGAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400	
Db	8341	CAGAGCTTGCACTGAGCGGAGTTTGGCCCACTGCACCTCCAGCCTAGGTGACAGAGTGAGA	8400	
Qy	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAGTGAAGTA	8460	
Db	8401	CTCCATCTCAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAAAAATAAGTGAAGTA	8460	
Qy	8461	TAGAGTATCTCATAGTTTGTGCTGATAGAACACAGTTTCAACCTCAGTCAATCTGACCG	8520	
Db	8461	TAGAGTATCTCATAGTTTGTGCTGATAGAACACAGTTTCAACCTCAGTCAATCTGACCG	8520	
Qy	8521	TTTGATACATCTCAGACACACATACATTCAGTAGTTTAGATGCCCTAGAATAAATAGAGAA	8580	
Db	8521	TTTGATACATCTCAGACACACATACATTCAGTAGTTTAGATGCCCTAGAATAAATAGAGAA	8580	
Qy	8581	GGAAGGATGGCTCTTCTTGTGTCATTTGTTTCTTCAGTGACGTTGAATCAGAT	8640	
Db	8581	GGAAGGATGGCTCTTCTTGTGTCATTTGTTTCTTCAGTGACGTTGAATCAGAT	8640	
Qy	8641	GAAGGGGAACAGCAGAAAAACAACCAACTGATCCTCAGCTGTGTCATCTTTTAAAGATC	8700	
Db	8641	GAAGGGGAACAGCAGAAAAACAACCAACTGATCCTCAGCTGTGTCATCTTTTAAAGATC	8700	
Qy	8701	CCTGAAGAGGTCCTGGAAATGTACTCCCTGTGCTCCTCTGTGTGCTCCTTTTGGCATTC	8760	
Db	8701	CCTGAAGAGGTCCTGGAAATGTACTCCCTGTGCTCCTCTGTGTGCTCCTTTTGGCATTC	8760	
Qy	8761	TTTCTTTGGACCTTACCAAGGACTGTAAATGGTGGGACGCTAGTGGCCCTGCTGGCC	8820	
Db	8761	TTTCTTTGGACCTTACCAAGGACTGTAAATGGTGGGACGCTAGTGGCCCTGCTGGCC	8820	
Qy	8821	TTACACACGGTGTCTCCCTTAGGCCAGTGCCTCTGGAGTCAGAACTCTGGTGGTATTTTC	8880	

Db 8821 TTCACACAGGTGTCCTCCCTAGGCCAGTGCCTCTGGAGTCAGAACTCTGTGTTATTTTC 8880
Qy 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGGATGGTATATATGAAAGCCACCAGTG 8940
Db 8881 CCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGGATGGTATATGAAAGCCACCAGTG 8940
Qy 8941 GCTTAGAGGATGCCAGGTCCTCCATGGAGCCACTGGGTTCCGGTGCACATTAATAAAA 9000
Db 8941 GCTTAGAGGATGCCAGGTCCTCCATGGAGCCACTGGGTTCCGGTGCACATTAATAAAA 9000
Qy 9001 AAAATCTAACCCAGACATTCAGGAATTCCTAGATTCTGGGAATACAGTTCACCATGTTCA 9060
Db 9001 AAAATCTAACCCAGACATTCAGGAATTCCTAGATTCTGGGAATACAGTTCACCATGTTCA 9060
Qy 9061 AAAGAGTCTTTTTTTTTTTTTTTTGGAGACTCTATTGCCAGGCTGGAGTGCAATGSCATGAT 9120
Db 9061 AAAGAGTCTTTTTTTTTTTTTTTTGGAGACTCTATTGCCAGGCTGGAGTGCAATGSCATGAT 9120
Qy 9121 CTCGGCTCACTGTAACCTCTGCCTCCAGGTTCAAGGGATTCCTGTCTCAGCCCTCCCA 9180
Db 9121 CTCGGCTCACTGTAACCTCTGCCTCCAGGTTCAAGGGATTCCTGTCTCAGCCCTCCCA 9180
Qy 9181 AGTAGCTGGGATTAACGGCTGCACCAACCATGCCGCTAAATTTTGTATTTTAGTAGA 9240
Db 9181 AGTAGCTGGGATTAACGGCTGCACCAACCATGCCGCTAAATTTTGTATTTTAGTAGA 9240
Qy 9241 GACAGGTTTACCAATGTTGGCCAGGTCGTCTCGAACTCTCCTGACCTCGTATCCGCC 9300
Db 9241 GACAGGTTTACCAATGTTGGCCAGGTCGTCTCGAACTCTCCTGACCTCGTATCCGCC 9300
Qy 9301 TGCTCGCCCTCCCAAGTCTGAGATTACAGGTGAGCCACCCTGCCAGCCGTCFAAA 9360
Db 9301 TGCTCGCCCTCCCAAGTCTGAGATTACAGGTGAGCCACCCTGCCAGCCGTCFAAA 9360
Qy 9361 AGAGTCTTAATATATATATACAGATGSCATGCTTTTACATTTATGTTTACATGCACTTG 9420
Db 9361 AGAGTCTTAATATATATATACAGATGSCATGCTTTTACATTTATGTTTACATGCACTTG 9420
Qy 9421 GCTGCATAAATGTTGACAAAGCATTCGTCTTGAAGGGCAGGTGCTCAGGATACCATAT 9480
Db 9421 GCTGCATAAATGTTGACAAAGCATTCGTCTTGAAGGGCAGGTGCTCAGGATACCATAT 9480
Qy 9481 ACAGCTCAGAAATTTCTCTTTAGGCATTAATAATTTTAGCAAGATATCTCATCTCTCTT 9540
Db 9481 ACAGCTCAGAAATTTCTCTTTAGGCATTAATAATTTTAGCAAGATATCTCATCTCTCTT 9540
Qy 9541 TTAACCATTTTCTTTTTTTTGTGTTAGAAAAGTTATGTAGAAAAAGTAATGTGATTT 9600
Db 9541 TTAACCATTTTCTTTTTTTTGTGTTAGAAAAGTTATGTAGAAAAAGTAATGTGATTT 9600
Qy 9601 ACCTCATTTGACAAAGCTATAAATGAATCAATTAAGCTGTTATTTAATTAGCCAG 9660
Db 9601 ACCTCATTTGACAAAGCTATAAATGAATCAATTAAGCTGTTATTTAATTAGCCAG 9660
Qy 9661 TGAAGAACTATTAAACATTTGATTTGATATCTGCATGATTTTATGAAAGTTCTTGTT 9720
Db 9661 TGAAGAACTATTAAACATTTGATTTGATATCTGCATGATTTTATGAAAGTTCTTGTT 9720
Qy 9721 TATACATTTAATAATGATATTGATTTGATATCTGCATGATTTTATGAAAGTTCTTGTT 9780
Db 9721 TATACATTTAATAATGATATTGATTTGATATCTGCATGATTTTATGAAAGTTCTTGTT 9780
Qy 9781 ATCTTGATATATACATTAATCGTTGTCATTTTGGAGACATTTATTTGCTTCTAAATTT 9840
Db 9781 ATCTTGATATATACATTAATCGTTGTCATTTTGGAGACATTTATTTGCTTCTAAATTT 9840
Qy 9841 CTTTACATTTTGTCTTACGGAATATTTTCACTCACTGGTAGCGGAATTAATCGTGT 9900
Db 9841 CTTTACATTTTGTCTTACGGAATATTTTCACTCACTGGTAGCGGAATTAATCGTGT 9900
Qy 9901 TCTTCACTTAGGACATTTGCTGCTAAGTTGTGAAGACATTTGTTATTTTACCAGCAAA 9960
Db 9901 TCTTCACTTAGGACATTTGCTGCTAAGTTGTGAAGACATTTGTTATTTTACCAGCAAA 9960

Qy 9961 CATTTCTGAAGCATATGACAAATTTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020
Db 9961 CATTTCTGAAGCATATGACAAATTTATTTCTCTCTTAATATCTTACTATACTGAAAGCAGA 10020
Qy 10021 CTGCTATAAGGCTTCACTTACTCTCTACCTCATRAGGAATATGTTACAAATTAATTTATTT 10080
Db 10021 CTGCTATAAGGCTTCACTTACTCTCTACCTCATRAGGAATATGTTACAAATTAATTTATTT 10080
Qy 10081 AGGTAAAGCATTTTGTGTTTATTTATTTTATTTTACCTCGGCTGAGATTTCAAGAAACACC 10140
Db 10081 AGGTAAAGCATTTTGTGTTTATTTATTTTATTTTACCTCGGCTGAGATTTCAAGAAACACC 10140
Qy 10141 CCAGTCTTCACAGTACACATTTCTACTAACACATTTACTTAAACATCAGCACTGTGGCT 10200
Db 10141 CCAGTCTTCACAGTACACATTTCTACTAACACATTTACTTAAACATCAGCACTGTGGCT 10200
Qy 10201 GTTAATTTTTTAAATAGAAATTTTAAAGTCTCTCATTTTCTTTCGGTGTTTTTTAAAGCTTAA 10260
Db 10201 GTTAATTTTTTAAATAGAAATTTTAAAGTCTCTCATTTTCTTTCGGTGTTTTTTAAAGCTTAA 10260
Qy 10261 TTTTCTGCTTTTATTCATAAATTTCTTAAGTCAACTACATTTGAAAAATCAAGACCTG 10320
Db 10261 TTTTCTGCTTTTATTCATAAATTTCTTAAGTCAACTACATTTGAAAAATCAAGACCTG 10320
Qy 10321 CATTTTAAATTTCTTATTCACCTCTGCAAAACCATTCACAAACCATGTTAGTAAGAGAA 10380
Db 10321 CATTTTAAATTTCTTATTCACCTCTGCAAAACCATTCACAAACCATGTTAGTAAGAGAA 10380
Qy 10381 GGGTGACACCTGGTGCCATAGGTAAATGTACACGGTGGTCCGGTGACCAAGATGCG 10440
Db 10381 GGGTGACACCTGGTGCCATAGGTAAATGTACACGGTGGTCCGGTGACCAAGATGCG 10440
Qy 10441 CGCTCAGGTTTCTCTGAAGTAAAGGAATAAAGAAATGGGTGGAGGGCGTGCCTGGAA 10500
Db 10441 CGCTCAGGTTTCTCTGAAGTAAAGGAATAAAGAAATGGGTGGAGGGCGTGCCTGGAA 10500
Qy 10501 ATCACTTGTAGAAAAAGCCCTGAAATTTGAGAAAAACAAAGAACTACTTTACCAG 10560
Db 10501 ATCACTTGTAGAAAAAGCCCTGAAATTTGAGAAAAACAAAGAACTACTTTACCAG 10560
Qy 10561 CTATTTGAATTTGCTGGAATTCAGGCCATTTGCTGAGCTGCCTGAACCTGGGAACACAG 10620
Db 10561 CTATTTGAATTTGCTGGAATTCAGGCCATTTGCTGAGCTGCCTGAACCTGGGAACACAG 10620
Qy 10621 AAGGAAAAACAACTCTGATATCATTTAGTCAAGTACAGAGGTGATTGAGGACTGC 10680
Db 10621 AAGGAAAAACAACTCTGATATCATTTAGTCAAGTACAGAGGTGATTGAGGACTGC 10680
Qy 10681 TGAGAGGTACAGGGCCAAATTTCTTATGTTTATTAATAATGTCATCTTATAACTGT 10740
Db 10681 TGAGAGGTACAGGGCCAAATTTCTTATGTTTATTAATAATGTCATCTTATAACTGT 10740
Qy 10741 CAGTATTTTATAAACATTTCTCAAACTCACACATTTTAAAAACAAAAACACTGTCTC 10800
Db 10741 CAGTATTTTATAAACATTTCTCAAACTCACACATTTTAAAAACAAAAACACTGTCTC 10800
Qy 10801 TAAATCCCCAAATTTTTCATAAAC 10825
Db 10801 TAAATCCCCAAATTTTTCATAAAC 10825

RESULT 11

US-09-503-444A-5
; Sequence 5, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gnirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta

Db	3121	TGTTGGCTGAGCAGGTAGATCATTTTGAGTGCAGAGTTTGAGACAAGCTTTGCCAACA	3180
Qy	3181	TGFTGAACCCCTACTACTAAAAATACAAAATTAGCCCTGGTGTGGTCGACGCGCT	3240
Db	3181	TGFTGAACCCCTACTACTAAAAATACAAAATTAGCCCTGGTGTGGTCGACGCGCT	3240
Qy	3241	ATAGTCCCAGSTTTTCAGAGGCTTAGFTAGGAGAATCCCTTGAACCCAGAGGTGCAGG	3300
Db	3241	ATAGTCCCAGSTTTTCAGAGGCTTAGFTAGGAGAATCCCTTGAACCCAGAGGTGCAGG	3300
Qy	3301	TTGCGFTAGCTGAGATTGTGCCACTGCACTCCAGCCCTGGGTGATGAGTGAAGACTCTGT	3360
Db	3301	TTGCGFTAGCTGAGATTGTGCCACTGCACTCCAGCCCTGGGTGATGAGTGAAGACTCTGT	3360
Qy	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTAATCTCAGGATTTGGG	3420
Db	3361	CTCAAAAAAAAAAAAAAAAAAAAAAAAAAACTCAAGGAATTAATCTCAGGATTTGGG	3420
Qy	3421	TCTAATTTGCCCTGAGCACCACTCTGAGTTCAACTACCATGCTAGACACACCTTTAAC	3480
Db	3421	TCTAATTTGCCCTGAGCACCACTCTGAGTTCAACTACCATGCTAGACACACCTTTAAC	3480
Qy	3481	ATTTTTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTTGGAAATAGAT	3540
Db	3481	ATTTTTAGAAATCCACAGCTTTAGTGGAGTCTGTCTAATCATGAGTATTTGGAAATAGAT	3540
Qy	3541	CTGGGGCAGTGAGGGGTGGAGCCACGTGTGGCAGAGAAAAGCACACAAGGAAGAGC	3600
Db	3541	CTGGGGCAGTGAGGGGTGGAGCCACGTGTGGCAGAGAAAAGCACACAAGGAAGAGC	3600
Qy	3601	ACCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAATGAGGA	3660
Db	3601	ACCAGGACTGTCTATATGGAAGAAAGACAGGACTGCAACTCACCTTTCACAAAATGAGGA	3660
Qy	3661	CCAGACACACTGATGGTATGATGATGCAGGCTGTGTGGAGCCTCAACATCTGCTGCC	3720
Db	3661	CCAGACACACTGATGGTATGATGATGCAGGCTGTGTGGAGCCTCAACATCTGCTGCC	3720
Qy	3721	CTCCTACTACACATGGTTAAGSCCTTGTGCTGTCTCCAGGTTTCACACTCTCTGCACATA	3780
Db	3721	CTCCTACTACACATGGTTAAGSCCTTGTGCTGTCTCCAGGTTTCACACTCTCTGCACATA	3780
Qy	3781	CCTCTCATGGTGCCTCAGACAGACCTGGTCTTTCTTCTGTTGAACTTTGGGCTA	3840
Db	3781	CCTCTCATGGTGCCTCAGACAGACCTGGTCTTTCTTCTGTTGAACTTTGGGCTA	3840
Qy	3841	CGTGGATGACCACTGTTCTGTTCTATGATNATGAGAGTCCCGCTGTGGAGCCCCGAAC	3900
Db	3841	CGTGGATGACCACTGTTCTGTTCTATGATNATGAGAGTCCCGCTGTGGAGCCCCGAAC	3900
Qy	3901	TCCATGGTTTCCASTAGAAATTCACGACAGATGTGGCTCGAGCTGAGTCAAGAGTCTGAA	3960
Db	3901	TCCATGGTTTCCASTAGAAATTCACGACAGATGTGGCTCGAGCTGAGTCAAGAGTCTGAA	3960
Qy	3961	AGGTGGGATACATGTTCACTGTTGACTPCTGSACTATTATGAAAATCACAAACACAG	4020
Db	3961	AGGTGGGATACATGTTCACTGTTGACTPCTGSACTATTATGAAAATCACAAACACAG	4020
Qy	4021	CAAGGFTATGTGAGAGGGGGCTCACCTTCCTGAGGTTGTCAAGCTTTTTCATCTTTTC	4080
Db	4021	CAAGGFTATGTGAGAGGGGGCTCACCTTCCTGAGGTTGTCAAGCTTTTTCATCTTTTC	4080
Qy	4081	ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGGAGCGGGAAGAGGAAG	4140
Db	4081	ATGCATCTTGAAGAAACAGCTGGAAGTCTGAGTCTTGTGGGAGCGGGAAGAGGAAG	4140
Qy	4141	GAATTTCTCTTCTGAGATCATTTTGTGCTTGGGGATGTGGAAATAGGGACCTATTTCCTT	4200
Db	4141	GAATTTCTCTTCTGAGATCATTTTGTGCTTGGGGATGTGGAAATAGGGACCTATTTCCTT	4200
Qy	4201	TGFTTGCAGTTAAAGGCTGGGGATTTTTTCAGAGTCCCCACACCCCTGCAGGTCATCCTG	4260
Db	4201	TGFTTGCAGTTAAAGGCTGGGGATTTTTTCAGAGTCCCCACACCCCTGCAGGTCATCCTG	4260

Qy	4261	GGCTGTGAAATGCAAGAAGACAAACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Db	4261	GGCTGTGAAATGCAAGAAGACAAACAGTACCGGAGGCTACTGGAAGTACGGGTATGATGGG	4320
Qy	4321	CAGGACCACTTGAATCTTGCCCTGACACACTGGATTCGGAGAGCAGCAGAAACCCAGGGCC	4380
Db	4321	CAGGACCACTTGAATCTTGCCCTGACACACTGGATTCGGAGAGCAGCAGAAACCCAGGGCC	4380
Qy	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCCACAAGATTCGGGGCCAGGCAGACAGGGCCCTAC	4440
Db	4381	TGGCCCAACCAAGCTGGAGTGGGAAGGCCACAAGATTCGGGGCCAGGCAGACAGGGCCCTAC	4440
Qy	4441	CTGGAGAGGAGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGAGCAGAGTGTTTTG	4500
Db	4441	CTGGAGAGGAGACTGCCCTGCACAGCTGCAGCAGTTCGTGGAGCTGGGAGCAGAGTGTTTTG	4500
Qy	4501	GACCAACAAGGTATGTTGGNAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560
Db	4501	GACCAACAAGGTATGTTGGNAACACACTTCTGCCCTATACTCTAGTGGCAGAGTGGAGG	4560
Qy	4561	AGSTTGCAGGGCCAGGAATCCCTGGTGGAGTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Db	4561	AGSTTGCAGGGCCAGGAATCCCTGGTGGAGTTCAGAGGTGGCTGAGGCTGTGTGCCTC	4620
Qy	- 4621	TCCAAATCTTGGGAAGGACTTCTCAATCTTAGAGTCTCTACCTTATAATTAGATGTA	4680
Db	4621	TCCAAATCTTGGGAAGGACTTCTCAATCTTAGAGTCTCTACCTTATAATTAGATGTA	4680
Qy	4681	TGAGACAGCCACAGTCATGGGTTTAATTTCTTCCATGCATATGGCTCAAAAGGAA	4740
Db	4681	TGAGACAGCCACAGTCATGGGTTTAATTTCTTCCATGCATATGGCTCAAAAGGAA	4740
Qy	4741	GTGTCTATGGCCCTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
Db	4741	GTGTCTATGGCCCTGCTTTTATTTAAACCAATAATCTTTTGTATATTTATACCTGTAA	4800
Qy	4801	AAATTCAGAAATGTCAAGGCGGGCAGGTGGCTCACCCCTGTATATCCAGCAGCTTTGGG	4860
Db	4801	AAATTCAGAAATGTCAAGGCGGGCAGGTGGCTCACCCCTGTATATCCAGCAGCTTTGGG	4860
Qy	4861	AGGCCGAGGCGGTGTGTCAAGAGTTCAGAGTTCAGACACGCGCTGACCAACATGTTGAA	4920
Db	4861	AGGCCGAGGCGGTGTGTCAAGAGTTCAGAGTTCAGACACGCGCTGACCAACATGTTGAA	4920
Qy	4921	ACCGCTCTCTAAAAAATACAAAATAGCTGGTCACAGTCATCGCACCTGTAGTCCCA	4980
Db	4921	ACCGCTCTCTAAAAAATACAAAATAGCTGGTCACAGTCATCGCACCTGTAGTCCCA	4980
Qy	4981	GCTAATTTGGAAGGCTGAGGCGAGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040
Db	4981	GCTAATTTGGAAGGCTGAGGCGAGAGCATCGCTTGAACCTGGGAAGCGGAAGTTCACATGA	5040
Qy	5041	GCCAAGATCGCGCACTTGCACTCCAGCCTFAGGCAGCAGTGGAGACTCCATCTTAAAAAA	5100
Db	5041	GCCAAGATCGCGCACTTGCACTCCAGCCTFAGGCAGCAGTGGAGACTCCATCTTAAAAAA	5100
Qy	5101	AAAAAANAANAANAAGAGAATTCAGAGATCTCAGCTATCATATGATACCCAGGACAAA	5160
Db	5101	AAAAAANAANAANAAGAGAATTCAGAGATCTCAGCTATCATATGATACCCAGGACAAA	5160
Qy	5161	ATATCAAGTGAAGGCACTTATCAGAGTGAAGAATCCCTTTAGGTTAAAAAGTTCTTTTCAT	5220
Db	5161	ATATCAAGTGAAGGCACTTATCAGAGTGAAGAATCCCTTTAGGTTAAAAAGTTCTTTTCAT	5220
Qy	5221	AGACATAGCAATTAATCAGTGAAGTACCTATCTTTACAAGTCCGCTCTCTATACATGC	5280
Db	5221	AGACATAGCAATTAATCAGTGAAGTACCTATCTTTACAAGTCCGCTCTCTATACATGC	5280
Qy	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340
Db	5281	CTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTTCAATGCACATAA	5340

[illegible]

Db	6421	TCTCAGAACCCAAATCTGTTAGGAAATGAAATTTGATACCAAGTAAATCTAGTTAAAGAG	6480
QY	6481	ACCCCATGAGGTCCTTAAGACGAGGCAAGCAAAATGCTTAGGGTGTCAAAGAAAGAAATG	6540
Db	6481	ACCCCATGAGGTCCTTAAGACGAGGCAAGCAAAATGCTTAGGGTGTCAAAGAAAGAAATG	6540
QY	6541	ATCACATTCAGCTGGGGATCAAGATAGAGCTTCTCGATCTTCAAGAGAGAGCTGATATCCA	6600
Db	6541	ATCACATTCAGCTGGGGATCAAGATAGAGCTTCTCGATCTTCAAGAGAGAGCTGATATCCA	6600
QY	6601	TTAGGTGAGGTTGAAGATGATGGGAGGCTTACACAGACGAGCAACCATGCCAAGTAGGA	6660
Db	6601	TTAGGTGAGGTTGAAGATGATGGGAGGCTTACACAGACGAGCAACCATGCCAAGTAGGA	6660
QY	6661	GAGTATAAGGCATCTCGGAGATTAGAATAATTAATCTACTGATCTTAACCTGAGTTGGCT	6720
Db	6661	GAGTATAAGGCATCTCGGAGATTAGAATAATTAATCTACTGATCTTAACCTGAGTTGGCT	6720
QY	6721	AGCTATCACTCAACCAATATGCAATTTACCCCTGAAACATCTGTGGTGTAGGGAAGA	6780
Db	6721	AGCTATCACTCAACCAATATGCAATTTACCCCTGAAACATCTGTGGTGTAGGGAAGA	6780
QY	6781	GAATCAGAAAGACCGCTCATACAGAGTCCAAAGGCTTTTGGGATATTGGGTTATGA	6840
Db	6781	GAATCAGAAAGACCGCTCATACAGAGTCCAAAGGCTTTTGGGATATTGGGTTATGA	6840
QY	6841	TCACATGGGGTGTCATTTGAAGATCCTAAGAAAGAGGACACAGATCTCCCTTATATGGT	6900
Db	6841	TCACATGGGGTGTCATTTGAAGATCCTAAGAAAGAGGACACAGATCTCCCTTATATGGT	6900
QY	6901	AATGTGTTGTTAAGAAATTTAGATGAGAGGTCAGGAGACACAGTTAGAAGCCAAATACAT	6960
Db	6901	AATGTGTTGTTAAGAAATTTAGATGAGAGGTCAGGAGACACAGTTAGAAGCCAAATACAT	6960
QY	6961	TTCCAGATGAGAGATAATGGTCTTGAATCCAAATAGTGCCACAGGCTTAAATTTGAGATGG	7020
Db	6961	TTCCAGATGAGAGATAATGGTCTTGAATCCAAATAGTGCCACAGGCTTAAATTTGAGATGG	7020
QY	7021	GTGAATGAGGAATAAAGAGAGAGAGAGAGGCAAGATGGTGCTTAGTTGTGATGCCCT	7080
Db	7021	GTGAATGAGGAATAAAGAGAGAGAGAGAGGCAAGATGGTGCTTAGTTGTGATGCCCT	7080
QY	7081	CTTTCTCTGGGCTCTTTGCTCCACAGGAGGACCATGGGACACFACGCTCTTAGCTGAACG	7140
Db	7081	CTTTCTCTGGGCTCTTTGCTCCACAGGAGGACCATGGGACACFACGCTCTTAGCTGAACG	7140
QY	7141	TGAGTGACACGAGGCTCGACACTCTGTGGGAAGAGAGACAAACTTAGAGACTCAAGA	7200
Db	7141	TGAGTGACACGAGGCTCGACACTCTGTGGGAAGAGAGACAAACTTAGAGACTCAAGA	7200
QY	7201	GGGAGTGCAATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGACCTTAACCATAGAAAT	7260
Db	7201	GGGAGTGCAATTTATGAGCTCTTCATGTTTTCAGGAGAGAGTTGACCTTAACCATAGAAAT	7260
QY	7261	GCCTGACGAACCTCTTGATTTTTCGCTTTCATTTCCCTCAAAAGATTTCCCAT	7320
Db	7261	GCCTGACGAACCTCTTGATTTTTCGCTTTCATTTCCCTCAAAAGATTTCCCAT	7320
QY	7321	TTAGGTTTCTGAGTTCTTGATGTCGGGTGATCCCTAGCTGTGACCTCTCCCTTGGAACTG	7380
Db	7321	TTAGGTTTCTGAGTTCTTGATGTCGGGTGATCCCTAGCTGTGACCTCTCCCTTGGAACTG	7380
QY	7381	TCTCTCTGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCCCTCCGTCACCTCAGAG	7440
Db	7381	TCTCTCTGAACCTCAAGCTGCATCTAGAGGCTTCCCTTCATTTCCCTCCGTCACCTCAGAG	7440
QY	7441	ACATACACCTATGTCATTTCCATTTTGGAAAGAGGACTCCCTTAAATTTGGGGA	7500
Db	7441	ACATACACCTATGTCATTTCCATTTTGGAAAGAGGACTCCCTTAAATTTGGGGA	7500
QY	7501	CTTACATGATTCATTTTAAACATGAGAAAGCTTTTGAACCCCTGGGACGTTGCTAGTCAT	7560
Db	7501	CTTACATGATTCATTTTAAACATGAGAAAGCTTTTGAACCCCTGGGACGTTGCTAGTCAT	7560

Db 7501 CTTACATGATTCAATTTAAACATCTGAGAAAAGCTTTGAACCCCTGGGAGCTGGCTAGTCAT 7560
Qy 7561 AACCTTACCAGATTTTACACATGATCTATGCATTTCTCTGACCCGTTCAACTTTTCTCT 7620
Db 7561 AACCTTACCAGATTTTACACATGATCTATGCATTTCTCTGACCCGTTCAACTTTTCTCT 7620
Qy 7621 TTGAATCCCTCTCTCTGTTTACCCAGTAACCTCATCTGTCAACCAAGCCCTTGGGATTTCTTC 7680
Db 7621 TTGAATCCCTCTCTCTGTTTACCCAGTAACCTCATCTGTCAACCAAGCCCTTGGGATTTCTTC 7680
Qy 7681 CATCTGATTTGATGTAGTTGACAGCTATGAAGGCTGTACACTGCACGAATGAAGAG 7740
Db 7681 CATCTGATTTGATGTAGTTGACAGCTATGAAGGCTGTACACTGCACGAATGAAGAG 7740
Qy 7741 GCACCTGTCCAGAAAAAGCATCGGCTATCTGTGGGTAGTATGATGGTGTCTTTTACG 7800
Db 7741 GCACCTGTCCAGAAAAAGCATCATGGCTATCTGTGGGTAGTATGATGGTGTCTTTTACG 7800
Qy 7801 AGGTAGGAGCAATATCTTTGAAGGGTTGTGAAGAGGTGTTTTTCTTAATGGCATGA 7860
Db 7801 AGGTAGGAGCAATATCTTTGAAGGGTTGTGAAGAGGTGTTTTTCTTAATGGCATGA 7860
Qy 7861 AGGTGTCATACAGATTGCAAAAGTTTAAATGGTGCCCTTCAATTTGGGATGCTACTAGTAT 7920
Db 7861 AGGTGTCATACAGATTGCAAAAGTTTAAATGGTGCCCTTCAATTTGGGATGCTACTAGTAT 7920
Qy 7921 TCCAGACCTGAAGAAACACAAATATTTTCTACCTGGTCTCTCTTGTCTGATATGAATA 7980
Db 7921 TCCAGACCTGAAGAAACACAAATATTTTCTACCTGGTCTCTCTTGTCTGATATGAATA 7980
Qy 7981 ATTATGATAAGGATGATAAAGCACCTTACTTCTGTGCCGACTCTTCTGAGCACCTACTTFA 8040
Db 7981 ATTATGATAAGGATGATAAAGCACCTTACTTCTGTGCCGACTCTTCTGAGCACCTACTTFA 8040
Qy 8041 CATGCAATTTACTGATGACATCTCTTACAAATTTCTATGAGATAGGTACTATTATCCCCAT 8100
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Qy 8101 TTCTTTTTTAAATGAAGAAAGTGAAGTGAAGCGGACGGTGGCTCACGCTGTAATCCC 8160
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RESULT 12
US-09-503-444A-7
; Sequence 7, Application US/09503444A
; Patent No. 6228594
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Galirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect Version 8
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/503,444A
; FILING DATE: 14-Feb-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/652,265
; FILING DATE: 23-May-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,673
; FILING DATE: 16-Apr-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/630,912
; FILING DATE: 04-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0088-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10825 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
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; LOCATION: 6040..6153, 7107..7147)
; OTHER INFORMATION: /product= "Hereditary Hemochromatosis
; OTHER INFORMATION: and 24d2 mutations"
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; LOCATION: 140..7319
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; OTHER INFORMATION: cDNA containing a combination of both
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; OTHER INFORMATION: 24d1 and 24d2 alleles
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; OTHER INFORMATION:
; OTHER INFORMATION: /label= 24d1
; US-09-503-444A-7

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Db	901	GGTTTCCACCTCAGACGAATGCGTTGGCGGTGGGGCGGGAAGAGTGGCGTTGGGGA	960
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; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724, 394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H. CONTIG"
US-08-724-394A-20

Query Match 100.0%; Score 10823; DB 2; Length 246240;
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; Patent No. 587237
GENERAL INFORMATION:
; APPLICANT: Feder, John N.
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; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereof
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
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; CITY: San Francisco
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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08724.394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A. 35,136
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; REFERENCE/DOCKET NUMBER: 017957-000100
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; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
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; FEATURE:
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; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

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Qy	9001	AAATCTAACCCAGGACATTCAGGAATGCTAGATCTCGGGAATCAGTTCACCATGTTCA	9060
Db	201304	AAATCTAACCCAGGACATTCAGGAATGCTAGATCTCGGGAATCAGTTCACCATGTTCA	201363
Qy	9061	AAAGAGTCCTTTTTTTTTTTTTCAGACTCTATTGCCAGGCTGGAGTCAATGGCATGAT	9120
Db	201364	AAAGAGTCCTTTTTTTTTTTTTCAGACTCTATTGCCAGGCTGGAGTCAATGGCATGAT	201423
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Qy	9301	TGCTCTGGCCTCCCAAGTGCTCAGATTTACAGGTGTGAGCCACCTGCCAGCGCTCAAA	9360
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Db	202444	CCAGTCTTCAAGTAACACATTTTCACTAACAACATTTTACTAAACATCAGCAACTGTGGCCT	202503
Qy	10201	GTTTAATTTTTTAAATAGAAATTTTAAGTGCTCATTTTCTTTCGGTGCTTTTAAAGCTTAA	10260
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Qy	10801	TAAATCCCAAAATTTTTCATAAAC	10825
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RESULT 15
US-08-724-394A-22
; Sequence 22, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Laufer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereeto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

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Đb 198244 TGAGGAGTAAATTATGCGAGTCAGATGAGATCTCTCTTTGTTAGGGGTGGCTGAGG 198303
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QY 6361 TTTGCAAGAGTGTTTAAGTGTAGTACAGGGGCTTTGAGGTTGAGAACTACTGTGGCTAT 6420
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Đb 198724 TCTCAGAACCCAAATCTGGTAGGAAATGAATTTGATAGCAAGTAAATGTAGTTAAAGAAG 198783
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Đb 198844 ATCAATTCAGCTGGGATCAAGATAGCCCTCTGGAATCTTGAAGGAGAACTGGATTCCA 198903
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Đb 199024 AGCTATCACTCACCATTATGCAATTTCTACCCCTGAAACATCTGTGGTGTAGGAAAGA 199083
QY 6781 GAATCAGAAAGAACCCAGCTCATACAGATCCCAAGGTCCTTTTGGGATATTGGGTTATGA 6840
Đb 199084 GAATCAGAAAGAACCCAGCTCATACAGATCCCAAGGTCCTTTTGGGATATTGGGTTATGA 199143
QY 6841 TCAGTGGGTGTCAATTGAAGGATCTTAAGAAAGGAGGACCAACGATCTCCCTTATATGGTG 6900
Đb 199144 TCAGTGGGTGTCAATTGAAGGATCTTAAGAAAGGAGGACCAACGATCTCCCTTATATGGTG 199203
QY 6901 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGGCCAGTTAGAAAGCCAATAGCAT 6960
Đb 199204 AATGTGTTGTTAAGAAGTTAGATGAGAGGTGAGGAGGCCAGTTAGAAAGCCAATAGCAT 199263
QY 6961 TTCAGATGAGAGATATGTTCTTTGAAATCCCAATAGTGCCCAAGGTCCTAAATGAGATGG 7020
Đb 199264 TTCAGATGAGAGATATGTTCTTTGAAATCCCAATAGTGCCCAAGGTCCTAAATGAGATGG 199323
QY 7021 GTGAATGAGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCC 7080
Đb 199324 GTGAATGAGAAATTAAGGAAGAGAGAGAGGCAAGATGGTGCCTAGGTTTGTGATGCC 199383

QY 7081 CTTTCTGGGTCTCTTGTCTCCACAGAGAGCCATGGGGCACTAGCTCTTAGCTGAACG 7140
Đb 199384 CTTTCTGGGTCTCTTGTCTCCACAGAGAGCCATGGGGCACTAGCTCTTAGCTGAACG 199443
QY 7141 TGAGTCACAGCGAGCTGCAGACTCACTGTGGGAAGAGACAAACTAGAGACTCAAGA 7200
Đb 199444 TGAGTCACAGCGAGCTGCAGACTCACTGTGGGAAGAGACAAACTAGAGACTCAAGA 199503
QY 7201 GGGAGTGCAATTTATGAGCTCTTTCATGTTTTAGAGAGAGTTTGAACCTTAAACATAGAAAT 7260
Đb 199504 GGGAGTGCAATTTATGAGCTCTTTCATGTTTTAGAGAGAGTTTGAACCTTAAACATAGAAAT 199563
QY 7261 GCCTGACGAACTCCTTGATTTAGCCCTTCTCTGTTTCATTTCTCAAAAAGATTTCCCAT 7320
Đb 199564 GCCTGACGAACTCCTTGATTTAGCCCTTCTCTGTTTCATTTCTCAAAAAGATTTCCCAT 199623
QY 7321 TTAGGTTTCTGAGTTTCTGCATGCCGCTGATCCCTAGCTGTGACCTCTCCCTGGAAC 7380
Đb 199624 TTAGGTTTCTGAGTTTCTGCATGCCGCTGATCCCTAGCTGTGACCTCTCCCTGGAAC 199683
QY 7381 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCTCCCTGACTCAGAG 7440
Đb 199684 TCTCTCATGAACCTCAAGCTGCATCTAGAGGCTTCCTTCATTTCTCTCCCTGACTCAGAG 199743
QY 7441 ACATACACCTATGTCATTTTCATTTTCCCTATTTTGGGAAGAGGACTCCTTAAATTTGGGGA 7500
Đb 199744 ACATACACCTATGTCATTTTCATTTTCCCTATTTTGGGAAGAGGACTCCTTAAATTTGGGGA 199803
QY 7501 CTTACATGATTCATTTTAACTCTGAGAAAAGCTTTGAAACCTGGGAGCTGGCTAGTCA 7560
Đb 199804 CTTACATGATTCATTTTAACTCTGAGAAAAGCTTTGAAACCTGGGAGCTGGCTAGTCA 199863
QY 7561 AACCTTACCAGATTTTACACATGATCTATGCAATTTCTGACCCGTTCAACTTTTCT 7620
Đb 199864 AACCTTACCAGATTTTACACATGATCTATGCAATTTCTGACCCGTTCAACTTTTCT 199923
QY 7621 TTGAATCCTCTCTCTGTGTACCCAGTAATCATCTGTGCACCAAGCTTTGGGATTTCT 7680
Đb 199924 TTGAATCCTCTCTCTGTGTACCCAGTAATCATCTGTGCACCAAGCTTTGGGATTTCT 199983
QY 7681 CATCTGATTTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCAGAAATGAAGAG 7740
Đb 199984 CATCTGATTTGTGATGTGAGTTGCACAGCTATGAAGGCTGTACACTGCAGAAATGAAGAG 200043
QY 7741 GCACCTGTCCCAGAAAAGCATCGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC 7800
Đb 200044 GCACCTGTCCCAGAAAAGCATCGCTATCTGTGGGTAGTATGATGGGTGTTTTAGC 200103
QY 7801 AGGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGTTGTTTCTTAATTTGGCATGA 7860
Đb 200104 AGGTAGGAGGCAAAATATCTTGAAGGGGTTGTGAAGAGGTTGTTTCTTAATTTGGCATGA 200163
QY 7861 AGGTGTACAGATTTGCAAAAGTTTAAATGGTCCCTCATTTGGGATGCTACTCTAGTAT 7920
Đb 200164 AGGTGTACAGATTTGCAAAAGTTTAAATGGTCCCTCATTTGGGATGCTACTCTAGTAT 200223
QY 7921 TCCAGACCTTGAAGAATCAATAATTTTCTACCTGGTCTCTCTCTGTTCTGATATGAA 7980
Đb 200224 TCCAGACCTTGAAGAATCAATAATTTTCTACCTGGTCTCTCTCTGTTCTGATATGAA 200283
QY 7981 ATTATGATAAGGATGATAAAGCACTTACTTGGTCTCCGACTCTTCTGAGCACCTACTT 8040
Đb 200284 ATTATGATAAGGATGATAAAGCACTTACTTGGTCTCCGACTCTTCTGAGCACCTACTT 200343
QY 8041 CATGATTACTGCATGCACTTCTTACATAATTTCTATCAGATAGGTACTATATTCGCCAT 8100
Đb 200344 CATGATTACTGCATGCACTTCTTACATAATTTCTATCAGATAGGTACTATATTCGCCAT 200403
QY 8101 TTTCTTTTAAATGAAGAAAGTGAAGTAGGGCGGGCAGGGTGGCTCAGCCCTGTAATCCC 8160
Đb 200404 TTTCTTTTAAATGAAGAAAGTGAAGTAGGGCGGGCAGGGTGGCTCAGCCCTGTAATCCC 200463

Qy	8161	AGCATT	TGGAGCCAAACGCGGTGGAT	TCAGAGGT	CAGGAGAT	TCGAGACCAT	CCTCTGGC	8220
Db	200464	AGCATT	TGGAGCCAAACGCGGTGGAT	TCAGAGGT	CAGGAGAT	TCGAGACCAT	CCTCTGGC	200523
Qy	8221	TACATGGT	GAAACCCCATCTCT	TAATAAAAT	TACAAAAAT	TAGCTGGCGTGGTGGCAG	8280	
Db	200524	TACATGGT	GAAACCCCATCTCT	TAATAAAAT	TACAAAAAT	TAGCTGGCGTGGTGGCAG	200583	
Qy	8281	ACGCTGT	AGTCTCCAGCTACT	TCGGAAGGCT	GAGGAGAA	TGCGATGA	CCCCAGGAGG	8340
Db	200584	ACGCTGT	AGTCTCCAGCTACT	TCGGAAGGCT	GAGGAGAA	TGCGATGA	CCCCAGGAGG	200643
Qy	8341	CAGAGT	TGCAAGTGGCGGAGTT	TGCGGCAC	TGCACTCCAGCCT	AGTGCACAGAGTGAGA	8400	
Db	200644	CAGAGT	TGCAAGTGGCGGAGTT	TGCGGCAC	TGCACTCCAGCCT	AGTGCACAGAGTGAGA	200703	
Qy	8401	CTCCAT	CTCAAAAAAT	TAAAAAT	TAAAAAT	TAAAAAT	TAAAAAT	8460
Db	200704	CTCCAT	CTCAAAAAAT	TAAAAAT	TAAAAAT	TAAAAAT	TAAAAAT	200763
Qy	8461	TAGAGT	ATCTCATAGTTT	GTCACTGAT	TAGAACAGG	TTTCAAAC	TCACTCAATCTGACCG	8520
Db	200764	TAGAGT	ATCTCATAGTTT	GTCACTGAT	TAGAACAGG	TTTCAAAC	TCACTCAATCTGACCG	200823
Qy	8521	TTTCAT	ACATCTCAGACACCACT	TACATTCAG	TAGTTT	TAGATGCCT	TAGATAAAT	8580
Db	200824	TTTCAT	ACATCTCAGACACCACT	TACATTCAG	TAGTTT	TAGATGCCT	TAGATAAAT	200883
Qy	8581	GGAAG	GAGATGGCTCTTCT	CTTGTCAT	TGTGTTTCT	TCTGAGTGAG	TTTGAATCAAT	8640
Db	200884	GGAAG	GAGATGGCTCTTCT	CTTGTCAT	TGTGTTTCT	TCTGAGTGAG	TTTGAATCAAT	200943
Qy	8641	GAGGG	ACAGCAGAGAAACCA	CACTGATCT	CAAGCTG	TCATGTTCT	TCTTTAAAGTC	8700
Db	200944	GAGGG	ACAGCAGAGAAACCA	CACTGATCT	CAAGCTG	TCATGTTCT	TCTTTAAAGTC	201003
Qy	8701	CCTGA	AGGAGGCTCTGGAAT	TGTACTCC	TCTGCTCT	CTGTTGCTCT	TTTGGCATCA	8760
Db	201004	CCTGA	AGGAGGCTCTGGAAT	TGTACTCC	TCTGCTCT	CTGTTGCTCT	TTTGGCATCA	201063
Qy	8761	TTTCT	TGGACCTTACCAAGG	ACTGTAAT	TGTTGGG	CAGCTAGTGC	CCCTGCTGGC	8820
Db	201064	TTTCT	TGGACCTTACCAAGG	ACTGTAAT	TGTTGGG	CAGCTAGTGC	CCCTGCTGGC	201123
Qy	8821	TTCAC	CACGGTGCTCCCT	CCTAGGCC	AGTGCCTCT	CGAGTCAG	AACCTGCTGGTATTC	8880
Db	201124	TTCAC	CACGGTGCTCCCT	CCTAGGCC	AGTGCCTCT	CGAGTCAG	AACCTGCTGGTATTC	201183
Qy	8881	CCTCA	ATGAAGTGAGTAAGCT	CTCTCAT	TTT	GAGATGCTAT	AATGGAAGCCACCAAGTG	8940
Db	201184	CCTCA	ATGAAGTGAGTAAGCT	CTCTCAT	TTT	GAGATGCTAT	AATGGAAGCCACCAAGTG	201243
Qy	8941	GCTT	AGAGATGCCAGGCT	CCCTCCAT	CTGAGCC	ACTGGGTTCCGGT	TGCACATATAAAAA	9000
Db	201244	GCTT	AGAGATGCCAGGCT	CCCTCCAT	CTGAGCC	ACTGGGTTCCGGT	TGCACATATAAAAA	201303
Qy	9001	AAAT	CTTAACAGGACAT	TCAGGAAT	TGCTAG	ATTCGGAAT	TCAGTTCAACATGTTCA	9060
Db	201304	AAAT	CTTAACAGGACAT	TCAGGAAT	TGCTAG	ATTCGGAAT	TCAGTTCAACATGTTCA	201363
Qy	9061	AAAG	AGTCTTTTTTTTTTT	TTTGTAG	ACTCTAT	TTCGCC	AGGCTGGAGTGC	9120
Db	201364	AAAG	AGTCTTTTTTTTTTT	TTTGTAG	ACTCTAT	TTCGCC	AGGCTGGAGTGC	201423
Qy	9121	CTCG	CTC	ACTGTAA	CCCTCTCC	AGGTTCA	AGGATTTCTCTG	9180
Db	201424	CTCG	CTC	ACTGTAA	CCCTCTCC	AGGTTCA	AGGATTTCTCTG	201483
Qy	9181	AGT	AGCTGG	GAATAC	AGCGGTGC	ACCACTG	CCCGCTAATTTT	9240
Db	201484	AGT	AGCTGG	GAATAC	AGCGGTGC	ACCACTG	CCCGCTAATTTT	201543
Qy	9241	GAC	AGGGTTT	CACAT	GTGTGG	CCAGGCTG	GTCTCGA	9300

Db	201544	 GACAGGGTTTACCATGTTGGCCAGGCTGGTCTCGAACTCTCTGACCTCGTATCCGCC	201603
Qy	9301	TGCGTCGGCCTCCCAAAGTCTCGAGATTCAGAGTGTGAGCCACCCCTGCCAGCGGTCAA	9360
Db	201604	TGCGTCGGCCTCCCAAAGTCTCGAGATTCAGAGTGTGAGCCACCCCTGCCAGCGGTCAA	201663
Qy	9361	AGAGTCCTTAATATATATATACAGATGGCATGTGTTTACTTTATGTTACTATACATGCACTTG	9420
Db	201664	AGAGTCCTTAATATATATATACAGATGGCATGTGTTTACTTTATGTTACTATACATGCACTTG	201723
Qy	9421	GCTGCATAAATGTGGTACAAGCATTCCTGCTTGAAGGGCAGGTGCTTCAGGATACCATAAT	9480
Db	201724	GCTGCATAAATGTGGTACAAGCATTCCTGCTTGAAGGGCAGGTGCTTCAGGATACCATAAT	201783
Qy	9481	ACAGCTCAGAAGTTTCCTTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTTT	9540
Db	201784	ACAGCTCAGAAGTTTCCTTTTAGGCAATTAATTTTAGCAAAAGATATCTCATCTCTCTTT	201843
Qy	9541	TTAAACCAATTTCTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT	9600
Db	201844	TTAAACCAATTTCTTTTTTGTGGTTAGAAAAGTTATGTAGAAAAAGTAAATGTGATTT	201903
Qy	9601	ACGCTCATTTGAGAAAAGCTATAAATGAATACAAATTAAGCTGTTATTTAATTAGCCAG	9660
Db	201904	ACGCTCATTTGAGAAAAGCTATAAATGAATACAAATTAAGCTGTTATTTAATTAGCCAG	201963
Qy	9661	TCGAAAACATTAACAACCTCTCTATTACCTGTTAGTATTATTGCTGCATTAATAATGCA	9720
Db	201964	TCGAAAACATTAACAACCTCTCTATTACCTGTTAGTATTATTGCTGCATTAATAATGCA	202023
Qy	9721	TATACCTTTAATAAATGTATATTGTTATGTAATGCAATGATTTTATTTGAAGTCTTGTTTC	9780
Db	202024	TATACCTTTAATAAATGTATATTGTTATGTAATGCAATGATTTTATTTGAAGTCTTGTTTC	202087
Qy	9781	ATCTTGTCGTATATCTTAATCGCTTGTGCATTTTGGAGACATTTATTTTGCCTCTCAATTT	9840
Db	202084	ATCTTGTCGTATATCTTAATCGCTTGTGCATTTTGGAGACATTTATTTTGCCTCTCAATTT	202147
Qy	9841	CTTTACATTTTGTCTTACGGAAATATTTTCATTCACATGTGGTAGCGGAAATTAATCGTGT	9900
Db	202144	CTTTACATTTTGTCTTACGGAAATATTTTCATTCACATGTGGTAGCGGAAATTAATCGTGT	202207
Qy	9901	TCCTTCACCTTAGGGACATGTGCTAAGTTGTGAAGACATTTGTTATTTTACCAGCAAC	9960
Db	202204	TCCTTCACCTTAGGGACATGTGCTAAGTTGTGAAGACATTTGTTATTTTACCAGCAAC	202266
Qy	9961	CATTCTGAAAGCATATGACAAATTAATTTCTCTTAATATCTTACTACTACTGAAAGCAGA	10020
Db	202264	CATTCTGAAAGCATATGACAAATTAATTTCTCTTAATATCTTACTACTACTGAAAGCAGA	202322
Qy	10021	CTGCTATAAGGCTTCACCTTACTCTTACCTCATGAAGGAATATGTTACAAATTAATTTAT	10080
Db	202324	CTGCTATAAGGCTTCACCTTACTCTTACCTCATGAAGGAATATGTTACAAATTAATTTAT	202387
Qy	10081	AGGTGAAGCATTTGTTTATATTGTTTATTTTCACTCGGCTGAGATTTCAAGAAACACC	10140
Db	202384	AGGTGAAGCATTTGTTTATATTGTTTATTTTCACTCGGCTGAGATTTCAAGAAACACC	202447
Qy	10141	CCAGTCTTCACAGTAACACATTTTCACTAACACATTTTACTAAACATCAGCACTGTGGCCT	10200
Db	202444	CCAGTCTTCACAGTAACACATTTTCACTAACACATTTTACTAAACATCAGCACTGTGGCCT	202507
Qy	10201	GTTAATTTTTTTAATAGAAATTTTAAGTCCTCATTTTCTTCGGTGTGTTTTTAAGCTTAA	10260
Db	202504	GTTAATTTTTTTAATAGAAATTTTAAGTCCTCATTTTCTTCGGTGTGTTTTTAAGCTTAA	202566
Qy	10261	TTTTTCTGGCTTTATTCATAAATCTTTAAGSTCAACTACATTTGAAAAATCAAGACCTG	10320
Db	202564	TTTTTCTGGCTTTATTCATAAATCTTTAAGSTCAACTACATTTGAAAAATCAAGACCTG	202627
Qy	10321	CATTTTAAATTTCTATTACCTCTTCGCAAAACCATTCACAAACCATGCTAGTAAGAGAA	10380

Db 202624 CATTTAAATCTTTATTACCTCTGGCAAAACCAATTCACAAACCATGGTAAAGAGAA 202683
QY 10381 GGGTGACACCTGGTGGCCATAGGTAAATGTACACCGGTGGTCCGGTGACCCAGAGATGCAG 10440
Db 202684 GGGTGACACCTGGTGGCCATAGGTAAATGTACACCGGTGGTCCGGTGACCCAGAGATGCAG 202743
QY 10441 CGCTGAGGGTTTTCTCTGAAGGTAAGGAATAAAGAAATGGGTGGAGGGCGGTGCACGTGAA 10500
Db 202744 CGCTGAGGGTTTTCTCTGAAGGTAAGGAATAAAGAAATGGGTGGAGGGCGGTGCACGTGAA 202803
QY 10501 ATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAAACAACAAGAACTACTTACCAG 10560
Db 202804 ATCACTTGTAGAGAAAGCCCTGAAATTTGAGAAAACAACAAGAACTACTTACCAG 202863
QY 10561 CTATTTGAATTCGCTGGAATCACAGGCCATTCCTGAGCTGCCTGAACTGGGAACACAAACAG 10620
Db 202864 CTATTTGAATTCGCTGGAATCACAGGCCATTCCTGAGCTGCCTGAACTGGGAACACAAACAG 202923
QY 10621 AAGGAAAACAACCACCTCTGATAATCATTTGAGTCAAGTACAGCAGGTGATTTGAGGACTGC 10680
Db 202924 AAGGAAAACAACCACCTCTGATAATCATTTGAGTCAAGTACAGCAGGTGATTTGAGGACTGC 202983
QY 10681 TGAGAGGTACAGGCCAAAATTCCTTATGTTGTTATTAATTAATGTCATCTTATAATACTGT 10740
Db 202984 TGAGAGGTACAGGCCAAAATTCCTTATGTTGTTATTAATTAATGTCATCTTATAATACTGT 203043
QY 10741 CAGTATTTTATAAAACATTCCTTCAAACTCACACACATTTAAAAACAACACACTGTCTC 10800
Db 203044 CAGTATTTTATAAAACATTCCTTCAAACTCACACACATTTAAAAACAACACACTGTCTC 203103
QY 10801 TAAATCCCCAAATTTTTCATAAAC 10825
Db 203104 TAAATCCCCAAATTTTTCATAAAC 203128

